

SEQUENCE LISTING

<110> Bejanin, Stephan  
Tanaka, Hiroaki

<120> HUMAN CDNAS AND PROTEINS AND USES THEREOF

<130> 142.US5.REG

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<150> 2001-08-10

<151> 60/311,305

<150> 2001-08-24

<151> 60/314,734

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 Glu Phe Ala Arg Ile Cys Arg Asp Leu Ser His Ile Gly Asp Ala Val  
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 Val Ile Ser Cys Ala Lys Asp Gly Val Lys Phe Ser Ala Ser Gly Glu  
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 Glu Glu Glu Ala Val Thr Ile Glu Met Asn Glu Pro Val Gln Leu Thr  
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 Phe Ala Leu Arg Tyr Leu Asn Phe Phe Thr Lys Ala Thr Pro Leu Ser  
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 Ser Thr Val Thr Leu Ser Met Ser Ala Asp Val Pro Leu Val Val Glu  
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tat aaa att gcg gat atg gga cac tta aaa tac tac ttg gct ccc aag 572  
 Tyr Lys Ile Ala Asp Met Gly His Leu Lys Tyr Tyr Leu Ala Pro Lys  
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 Ile Glu Asp Glu Glu Gly Ser  
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Asn Val Asp Lys Glu Glu Glu Ala Val Thr Ile Glu Met Asn Glu Pro  
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Val Gln Leu Thr Phe Ala Leu Arg Tyr Leu Asn Phe Phe Thr Lys Ala  
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Leu	Leu	Lys	Ile	Asp	Asn	Arg	Asn
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Thr	His	Leu	Ile	Arg	Trp	Val	Gly
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Val	Trp	Lys	Trp	Glu	Asp	Gly	Ser
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Phe	Leu	Glu	Asp	Gly	Lys	Gly	Asn
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Tyr	Cys
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Ile	Val
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Leu	Ser
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Gln	Tyr	Trp	Asp	Ser	Thr	Ile	Ser	Ser	Gly	Leu	Cys	Ile	Gln	Pro
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Pro	Tyr	Pro	Gly	Asn	Ile	Phe	Arg	Leu	Lys	Tyr	Cys	Gly	Asn	Leu
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Lys	Asp	Pro	Cys	Cys	Leu	Leu	Asn	Cys	Thr	Leu	His	Pro	Gly	Ala
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Asn	Gly	Thr	Ser	His	Gln	Cys	Pro	Asp	Asp	Val	Tyr	Val	Gln	Asp
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His	Asp	Ile	Gln	Cys	Lys	Glu	Ile	Phe	Gly	Gln	Asp	Ala	Arg	Ser
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atc atg gac agg atg aca gtg agc acg ctg gtg ctg gga gag ggc gct 485  
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Ala Tyr Glu Lys Thr Asp Thr Asp Gly Lys Phe Leu Tyr His Lys Ser  
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Lys Trp Asn Ile Thr Met Glu Ser Tyr Val Val His Thr Asn Tyr Asp  
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Glu Tyr Ala Ile Phe Leu Thr Lys Lys Phe Ser Arg His His Gly Pro  
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Thr Ile Thr Ala Lys Leu Tyr Gly Arg Ala Pro Gln Leu Arg Glu Thr  
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Leu Leu Gln Asp Phe Arg Val Val Ala Gln Gly Val Gly Ile Pro Glu  
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Asp Ser Ile Phe Thr Met Ala Asp Arg Gly Glu Cys Val Pro Gly Glu  
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Gln Glu Pro Glu Pro Ile Leu Ile Pro Arg Val Arg Arg Ala Ala Thr  
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 Phe Lys Asp Thr Thr Pro Asp Glu Leu Leu Ser Ala Val Met Thr Ala  
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 1 5 10  
 Cys Arg Ala Gly Arg Gly Gly Phe Lys Asp Thr Thr Pro Asp Glu Leu  
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 Glu Gln Leu Gly Asp Ile Cys Val Gly Asn Val Leu Gln Pro Gly Ala  
 50 55 60  
 Gly Ala Ile Met Ala Arg Ile Ala Gln Phe Leu Ser Asp Ile Pro Glu  
 65 70 75  
 Thr Val Pro Leu Ser Thr Val Asn Arg Gln Cys Ser Ser Gly Leu Gln  
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 Cys Ser Leu Gln Asn Ala Gln Glu Ala Leu Ile Val Thr Trp Gln Lys  
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 70 75 80  
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Val Thr Ser Ile Leu His Ile Lys Asp Pro Lys Asn Gln Val Gly Lys						
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gag gtg atc tgc cag gtg ctg cac ctg ggg act gtg acc gac ttt aag						857
Glu Val Ile Cys Gln Val Leu His Leu Gly Thr Val Thr Asp Phe Lys						
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Ile Val Ser Leu Val Ile Leu Leu Val Leu Ile Ser Ile Leu Leu Tyr						
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Gly	Tyr	Trp	Phe	Ser	Val	Pro	Leu	Leu	Leu	Ser	Ile	Val	Ser	Leu	Val	
			205				210					215				
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Gly Leu Ala Ser Ala Asn Val Asp Phe Ala Leu Ser Leu Tyr Lys Gln
      25                    30                    35                    40

tta gtc ctg aag gcc cct gat aag aat gtc atc ttc tcc cca ctg agc 302
Leu Val Leu Lys Ala Pro Asp Lys Asn Val Ile Phe Ser Pro Leu Ser
            45                    50                    55

atc tcc acc gcc ttg gcc ttc ctg tct ctg ggg gcc cat aat acc acc 350
Ile Ser Thr Ala Leu Ala Phe Leu Ser Leu Gly Ala His Asn Thr Thr
            60                    65                    70

ctg aca gag att ctc aaa ggc ctc aag ttc aac ctc acg gag act tct 398
Leu Thr Glu Ile Leu Lys Gly Leu Lys Phe Asn Leu Thr Glu Thr Ser
            75                    80                    85

gag gca gaa att cac cag agc ttc cag cac ctc ctg cgc acc ctc aat 446
Glu Ala Glu Ile His Gln Ser Phe Gln His Leu Leu Arg Thr Leu Asn
            90                    95                    100

cag tcc agc gat gag ctg cag ctg agt atg gga aat gcc atg ttt gtc 494
Gln Ser Ser Asp Glu Leu Gln Leu Ser Met Gly Asn Ala Met Phe Val
      105                    110                    115                    120

aaa gag caa ctc agt ctg ctg gac agg ttc acg gag gat gcc aag agg 542
Lys Glu Gln Leu Ser Leu Leu Asp Arg Phe Thr Glu Asp Ala Lys Arg
            125                    130                    135

ctg tat ggc tcc gag gcc ttt gcc act gac ttt cag gac tca gct gca 590
Leu Tyr Gly Ser Glu Ala Phe Ala Thr Asp Phe Gln Asp Ser Ala Ala
            140                    145                    150

gct aag aag ctc atc aac gac tac gtg aag aat gga act agg ggg aaa 638
Ala Lys Lys Leu Ile Asn Asp Tyr Val Lys Asn Gly Thr Arg Gly Lys
            155                    160                    165

atc aca gat ctg atc aag gac ctt gac tcg cag aca atg atg gtc ctg 686
Ile Thr Asp Leu Ile Lys Asp Leu Asp Ser Gln Thr Met Met Val Leu
            170                    175                    180

gtg aat tac atc ttc ttt aaa gcc aaa tgg gag atg ccc ttt gac ccc 734
Val Asn Tyr Ile Phe Phe Lys Ala Lys Trp Glu Met Pro Phe Asp Pro
      185                    190                    195                    200

caa gat act cat cag tca agg ttc tac ttg agc aag aaa aag tgg gta 782
Gln Asp Thr His Gln Ser Arg Phe Tyr Leu Ser Lys Lys Lys Trp Val
            205                    210                    215

atg gtg ccc atg atg agt ttg cat cac ctg act ata cct tac ttc cgg 830
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Met	Val	Pro	Met	Met	Ser	Leu	His	His	Leu	Thr	Ile	Pro	Tyr	Phe	Arg	
			220					225					230			
gac	gag	gag	ctg	tcc	tgc	acc	gtg	gtg	gag	ctg	aag	tac	aca	ggc	aat	878
Asp	Glu	Glu	Leu	Ser	Cys	Thr	Val	Val	Glu	Leu	Lys	Tyr	Thr	Gly	Asn	
		235					240				245					
gcc	agc	gca	ctc	ttc	atc	ctc	cct	gat	caa	gac	aag	atg	gag	gaa	gtg	926
Ala	Ser	Ala	Leu	Phe	Ile	Leu	Pro	Asp	Gln	Asp	Lys	Met	Glu	Glu	Val	
	250					255					260					
gaa	gcc	atg	ctg	ctc	cca	gag	acc	ctg	aag	cgg	tgg	aga	gac	tct	ctg	974
Glu	Ala	Met	Leu	Leu	Pro	Glu	Thr	Leu	Lys	Arg	Trp	Arg	Asp	Ser	Leu	
265					270				275						280	
gag	ttc	aga	gag	ata	ggg	gag	ctc	tac	ctg	cca	aag	ttt	tcc	atc	tcg	1022
Glu	Phe	Arg	Glu	Ile	Gly	Glu	Leu	Tyr	Leu	Pro	Lys	Phe	Ser	Ile	Ser	
			285					290						295		
agg	gac	tat	aac	ctg	aac	gac	ata	ctt	ctc	cag	ctg	ggc	att	gag	gaa	1070
Arg	Asp	Tyr	Asn	Leu	Asn	Asp	Ile	Leu	Leu	Gln	Leu	Gly	Ile	Glu	Glu	
		300					305					310				
gcc	ttc	acc	agc	aag	gct	gac	ctg	tca	ggg	atc	aca	ggg	gcc	agg	aac	1118
Ala	Phe	Thr	Ser	Lys	Ala	Asp	Leu	Ser	Gly	Ile	Thr	Gly	Ala	Arg	Asn	
	315					320					325					
cta	gca	gtc	tcc	cag	gtg	gtc	cat	aag	gct	gtg	ctt	gat	gta	ttt	gag	1166
Leu	Ala	Val	Ser	Gln	Val	Val	His	Lys	Ala	Val	Leu	Asp	Val	Phe	Glu	
	330				335					340						
gag	ggc	aca	gaa	gca	tct	gct	gcc	aca	gca	gtc	aaa	atc	acc	ctc	ctt	1214
Glu	Gly	Thr	Glu	Ala	Ser	Ala	Ala	Thr	Ala	Val	Lys	Ile	Thr	Leu	Leu	
345				350					355						360	
tct	gca	tta	gtg	gag	aca	agg	acc	att	gtg	cgt	ttc	aac	agg	ccc	ttc	1262
Ser	Ala	Leu	Val	Glu	Thr	Arg	Thr	Ile	Val	Arg	Phe	Asn	Arg	Pro	Phe	
			365				370						375			
ctg	atg	atc	att	gtc	cct	aca	gac	acc	cag	aac	atc	ttc	ttc	atg	agc	1310
Leu	Met	Ile	Ile	Val	Pro	Thr	Asp	Thr	Gln	Asn	Ile	Phe	Phe	Met	Ser	
		380					385				390					
aaa	gtc	acc	aat	ccc	aag	caa	gcc	tagagcttg	catcaagcag	tggggctctc						1364
Lys	Val	Thr	Asn	Pro	Lys	Gln	Ala									
	395				400											
agtaaggaac	ttggaatgca	agctggatgc	ctgggtctct	gggcacagcc	tggeccctgt											1424
gcaccgagtg	gccatggcat	gtgtggccct	gtctgcttat	ccttggaagg	tgacagcgat											1484
tcctgtgta	gctctcacat	gcacaggggc	ccatggactc	ttcagtcctgg	agggtcctgg											1544
gcctcctgac	agcaataaat	aatttcgttg	gacacgcaaa	aaaaaaaaaa	aaa											1597

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 <212> PRT  
 <213> Homo sapiens

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 <222> 1..23

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 Phe Cys Pro Ala Val Leu Cys His Pro Asn Ser Pro Leu Asp Glu Glu  
 -5 1 5

Asn	Leu	Thr	Gln	Glu	Asn	Gln	Asp	Arg	Gly	Thr	His	Val	Asp	Leu	Gly
10					15					20					25
Leu	Ala	Ser	Ala	Asn	Val	Asp	Phe	Ala	Leu	Ser	Leu	Tyr	Lys	Gln	Leu
				30					35					40	
Val	Leu	Lys	Ala	Pro	Asp	Lys	Asn	Val	Ile	Phe	Ser	Pro	Leu	Ser	Ile
			45					50					55		
Ser	Thr	Ala	Leu	Ala	Phe	Leu	Ser	Leu	Gly	Ala	His	Asn	Thr	Thr	Leu
		60					65					70			
Thr	Glu	Ile	Leu	Lys	Gly	Leu	Lys	Phe	Asn	Leu	Thr	Glu	Thr	Ser	Glu
	75					80					85				
Ala	Glu	Ile	His	Gln	Ser	Phe	Gln	His	Leu	Leu	Arg	Thr	Leu	Asn	Gln
90					95					100					105
Ser	Ser	Asp	Glu	Leu	Gln	Leu	Ser	Met	Gly	Asn	Ala	Met	Phe	Val	Lys
				110					115					120	
Glu	Gln	Leu	Ser	Leu	Leu	Asp	Arg	Phe	Thr	Glu	Asp	Ala	Lys	Arg	Leu
			125					130					135		
Tyr	Gly	Ser	Glu	Ala	Phe	Ala	Thr	Asp	Phe	Gln	Asp	Ser	Ala	Ala	Ala
		140					145					150			
Lys	Lys	Leu	Ile	Asn	Asp	Tyr	Val	Lys	Asn	Gly	Thr	Arg	Gly	Lys	Ile
	155					160					165				
Thr	Asp	Leu	Ile	Lys	Asp	Leu	Asp	Ser	Gln	Thr	Met	Met	Val	Leu	Val
170					175					180					185
Asn	Tyr	Ile	Phe	Phe	Lys	Ala	Lys	Trp	Glu	Met	Pro	Phe	Asp	Pro	Gln
				190					195					200	
Asp	Thr	His	Gln	Ser	Arg	Phe	Tyr	Leu	Ser	Lys	Lys	Lys	Trp	Val	Met
		205						210					215		
Val	Pro	Met	Met	Ser	Leu	His	His	Leu	Thr	Ile	Pro	Tyr	Phe	Arg	Asp
		220					225					230			
Glu	Glu	Leu	Ser	Cys	Thr	Val	Val	Glu	Leu	Lys	Tyr	Thr	Gly	Asn	Ala
		235				240					245				
Ser	Ala	Leu	Phe	Ile	Leu	Pro	Asp	Gln	Asp	Lys	Met	Glu	Glu	Val	Glu
250					255					260					265
Ala	Met	Leu	Leu	Pro	Glu	Thr	Leu	Lys	Arg	Trp	Arg	Asp	Ser	Leu	Glu
				270					275					280	
Phe	Arg	Glu	Ile	Gly	Glu	Leu	Tyr	Leu	Pro	Lys	Phe	Ser	Ile	Ser	Arg
			285					290					295		
Asp	Tyr	Asn	Leu	Asn	Asp	Ile	Leu	Gln	Leu	Gly	Ile	Glu	Glu	Ala	
		300					305				310				
Phe	Thr	Ser	Lys	Ala	Asp	Leu	Ser	Gly	Ile	Thr	Gly	Ala	Arg	Asn	Leu
		315				320					325				
Ala	Val	Ser	Gln	Val	Val	His	Lys	Ala	Val	Leu	Asp	Val	Phe	Glu	Glu
330					335					340					345
Gly	Thr	Glu	Ala	Ser	Ala	Ala	Thr	Ala	Val	Lys	Ile	Thr	Leu	Leu	Ser
				350					355					360	
Ala	Leu	Val	Glu	Thr	Arg	Thr	Ile	Val	Arg	Phe	Asn	Arg	Pro	Phe	Leu
			365					370					375		
Met	Ile	Ile	Val	Pro	Thr	Asp	Thr	Gln	Asn	Ile	Phe	Phe	Met	Ser	Lys
		380					385					390			
Val	Thr	Asn	Pro	Lys	Gln	Ala									
		395				400									

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 <212> DNA

<213> Homo sapiens

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<221> 5'UTR

<222> 1..152

<220>

<221> CDS

<222> 153..806

<220>

<221> 3'UTR

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<222> 1362..1367

<220>

<221> polyA\_site

<222> 1382..1397

<400> 15

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cgggcgcaaaa ggcaccaggg ccgcgccagg gcgcctcgca gcacggcctt gggggttctg 120
cgggccttcg ggtgcgcgtc tcgcctctag cc atg ggg tcc gca gcg ttg gag 173
                               Met Gly Ser Ala Ala Leu Glu
                               1 5
atc ctg ggc ctg gtg ctg tgc ctg gtg ggc tgg ggg ggt ctg atc ctg 221
Ile Leu Gly Leu Val Leu Cys Leu Val Gly Trp Gly Gly Leu Ile Leu
    10 15 20
gcg tgc ggg ctg ccc atg tgg cag gtg acc gcc ttc ctg gac cac aac 269
Ala Cys Gly Leu Pro Met Trp Gln Val Thr Ala Phe Leu Asp His Asn
    25 30 35
atc gtg acg gcg cag acc acc tgg aag ggg ctg tgg atg tcg tgc gtg 317
Ile Val Thr Ala Gln Thr Thr Trp Lys Gly Leu Trp Met Ser Cys Val
    40 45 50 55
gtg cag agc acc ggg cac atg cag tgc aaa gtg tac gac tcg gtg ctg 365
Val Gln Ser Thr Gly His Met Gln Cys Lys Val Tyr Asp Ser Val Leu
    60 65 70
gct ctg agc acc gag gtg cag gcg gcg cgg gcg ctc acc gtg agc gcc 413
Ala Leu Ser Thr Glu Val Gln Ala Ala Arg Ala Leu Thr Val Ser Ala
    75 80 85
gtg ctg ctg gcg ttc gtt gcg ctc ttc gtg acc ctg gcg ggc gcg cag 461
Val Leu Leu Ala Phe Val Ala Leu Phe Val Thr Leu Ala Gly Ala Gln
    90 95 100
tgc acc acc tgc gtg gcc ccg ggc ccg gcc aag gcg cgt gtg gcc ctc 509
Cys Thr Thr Cys Val Ala Pro Gly Pro Ala Lys Ala Arg Val Ala Leu
    105 110 115
acg gga ggc gtg ctc tac ctg ttt tgc ggg ctg ctg gcg ctc gtg cca 557
Thr Gly Gly Val Leu Thr Leu Phe Cys Gly Leu Leu Ala Leu Val Pro
    120 125 130 135
ctc tgc tgg ttc gcc aac att gtc gtc cgc gag ttt tac gac ccg tct 605
Leu Cys Trp Phe Ala Asn Ile Val Val Arg Glu Phe Tyr Asp Pro Ser
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	140		145		150	
gtg ccc gtg tgc cag aag tac gag ctg ggc gca gcg ctg tac atc ggc						653
Val Pro Val Ser Gln Lys Tyr Glu Leu Gly Ala Ala Leu Tyr Ile Gly						
	155		160		165	
tgg gcg gcc acc gcg ctg ctc atg gta ggc ggc tgc ctc ttg tgc tgc						701
Trp Ala Ala Thr Ala Leu Leu Met Val Gly Gly Cys Leu Leu Cys Cys						
	170		175		180	
ggc gcc tgg gtc tgc acc ggc cgt ccc gac ctc agc ttc ccc gtg aag						749
Gly Ala Trp Val Cys Thr Gly Arg Pro Asp Leu Ser Phe Pro Val Lys						
	185		190		195	
tac tca gcg ccg cgg cgg ccc acg gcc acc ggc gac aac gac aag aag						797
Tyr Ser Ala Pro Arg Arg Pro Thr Ala Thr Gly Asp Asn Asp Lys Lys						
200	205		210		215	
aac tac gtc tgagggcgct gggcacggcc gggccccctcc tgccagccac						846
Asn Tyr Val						
gcctgcgagg cgttggataa gcctggggag ccccgcatgg accgaggctt ccgcccgggta						906
gcgcgggcgcg caggcttctc ggaacgtccg gctctgcgcc ccgacgcggc tccctggatcc						966
gctcctgcct gcgcccgcag ctgaccttct cctgccacta gcccgccct gcccttaaca						1026
gacggaatga agtttcttct tctgtgcgcg gcgctgttct cataggcaga gcgggtgtca						1086
gactgaggat ttgccttccc ctccaagacg ctgggggtct tggctgctgc cttacttccc						1146
agaggctcct gctgacttcg gaggggcgga tgcagagccc agggccccca ccggaagatg						1206
tgtacagctg gtctttactc catcggcagg gcccgagccc agggaccagt gacttggcct						1266
ggacctcccg gtctcactcc agcatctccc caggcaaggc ttgtgggcac cggagcttga						1326
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aaaaaaaaa a						1397

<210> 16

<211> 218

<212> PRT

<213> Homo sapiens

<400> 16

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1		5				10					15					
Gly Trp Gly Gly Leu Ile Leu Ala Cys Gly Leu Pro Met Trp Gln Val																
	20					25					30					
Thr Ala Phe Leu Asp His Asn Ile Val Thr Ala Gln Thr Thr Trp Lys																
	35					40					45					
Gly Leu Trp Met Ser Cys Val Val Gln Ser Thr Gly His Met Gln Cys																
	50					55					60					
Lys Val Tyr Asp Ser Val Leu Ala Leu Ser Thr Glu Val Gln Ala Ala																
65						70					75					80
Arg Ala Leu Thr Val Ser Ala Val Leu Leu Ala Phe Val Ala Leu Phe																
	85										90					95
Val Thr Leu Ala Gly Ala Gln Cys Thr Thr Cys Val Ala Pro Gly Pro																
	100										105					110
Ala Lys Ala Arg Val Ala Leu Thr Gly Gly Val Leu Tyr Leu Phe Cys																
	115										120					125
Gly Leu Leu Ala Leu Val Pro Leu Cys Trp Phe Ala Asn Ile Val Val																
	130															
Arg Glu Phe Tyr Asp Pro Ser Val Pro Val Ser Gln Lys Tyr Glu Leu																
145						150					155					160
Gly Ala Ala Leu Tyr Ile Gly Trp Ala Ala Thr Ala Leu Leu Met Val																
	165										170					175

Gly Gly Cys Leu Leu Cys Cys Gly Ala Trp Val Cys Thr Gly Arg Pro  
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 Asp Leu Ser Phe Pro Val Lys Tyr Ser Ala Pro Arg Arg Pro Thr Ala  
 195 200 205  
 Thr Gly Asp Asn Asp Lys Lys Asn Tyr Val  
 210 215

<210> 17  
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 <212> DNA  
 <213> Homo sapiens

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 <222> 1..62

<220>  
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 <222> 63..572

<220>  
 <221> 3'UTR  
 <222> 573..782

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 <222> 750..755

<220>  
 <221> polyA\_site  
 <222> 767..782

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 ga atg cgg ctt caa ggg gct atc ttt gtg ctc ctg ccc cac ctg ggg 107  
 Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly  
 1 5 10 15  
 ccc atc ctg gtc tgg ctg ttc act cgt gat cac atg tct ggt tgg tgt 155  
 Pro Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys  
 20 25 30  
 gag ggc ccg agg atg ctg tcc tgg tgc cca ttc tac aaa gtc tta ttg 203  
 Glu Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu  
 35 40 45  
 ctt gta cag aca gcc atc tac tct gtc gtg ggc tat gcc tcc tac ctg 251  
 Leu Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu  
 50 55 60  
 gtg tgg aag gac ctg gga ggg ggc ttg ggg tgg ccc ctg gcc ctg cct 299  
 Val Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro  
 65 70 75  
 ctt ggc ctc tat gct gat cag ctc acc atc agc tgg act gtc ctg gtt 347  
 Leu Gly Leu Tyr Ala Asp Gln Leu Thr Ile Ser Trp Thr Val Leu Val  
 80 85 90 95  
 ctc ttt ttc aca gtc cac aac cct ggt ctg gcc ctg ctg cac ctg ctg 395  
 Leu Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu

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          100          105          110
ctg ctg tat ggg ctg gtg gtg agc aca gca ctg atc tgg cat ccc atc 443
Leu Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile
          115          120          125
aac aaa ctg gct gcc ctg tta ctg ctg ccc tac cta gcc tgg ctc acc 491
Asn Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr
          130          135          140
gtg act tca gcc ctc acc tac cac ctg tgg agg gac agc ctt tgt cca 539
Val Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro
          145          150          155
gtg cac cag cct cag ccc acg gag aag agt gac tgaggcccta gggcatggga 592
Val His Gln Pro Gln Pro Thr Glu Lys Ser Asp
          160          165          170
gaggagggac gcccaggggtg gggaggaaga gtctgcaagc agggctgtgg agttaggggt 652
cacccaatg ggaccaccct cctgggtccc ctgggtgccgt ttttccttag aaatcagaga 712
aatgggaaaag ggggggaaac tgattttaca cttaaataat aaaatcctat tagtaaaaaa 772
aaaaaaaaa 782

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<210> 18  
 <211> 170  
 <212> PRT  
 <213> Homo sapiens

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Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys Glu
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Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu Leu
          35          40          45
Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu Val
          50          55          60
Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro Leu
65          70          75          80
Gly Leu Tyr Ala Asp Gln Leu Thr Ile Ser Trp Thr Val Leu Val Leu
          85          90          95
Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu Leu
          100          105          110
Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile Asn
          115          120          125
Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr Val
          130          135          140
Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro Val
145          150          155          160
His Gln Pro Gln Pro Thr Glu Lys Ser Asp
          165          170

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<210> 19  
 <211> 789  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR



<222> 1..62

<220>

<221> CDS

<222> 63..572

<220>

<221> 3'UTR

<222> 573..789

<220>

<221> polyA\_signal

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ga atg cgg ctt caa ggg gct atc ttt gtg ctc ctg ccc cac ctg ggg 107

Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly

1 5 10 15

ccc atc ctg gtc tgg ctg ttc act cgt gat cac atg tct ggt ttg tgt 155

Pro Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Leu Cys

20 25 30

gag ggc ccg agg atg ctg tcc tgg tgc cca ttc tac aaa gtc tta ttg 203

Glu Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu

35 40 45

ctt gta cag aca gcc atc tac tct gtc gtg ggc tat gcc tcc tac ctg 251

Leu Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu

50 55 60

gtg tgg aag gac ctg gga ggg ggc ttg ggg tgg ccc ctg gcc ctg cct 299

Val Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro

65 70 75

ctt ggc ctc tat gct gtt cag ctg acc atc agc tgg act gtc ctg gtt 347

Leu Gly Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val

80 85 90 95

ctc ttt ttc aca gtc cac aac cct ggt ctg gcc ctg ctg cac ctg ctg 395

Leu Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu

100 105 110

ctg ctg tat ggg ctg gtg gtg agc aca gca ctg atc tgg cat ccc atc 443

Leu Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile

115 120 125

aac aaa ctg gct gcc ctg tta ctg ctg ccc tac cta gcc tgg ctc acc 491

Asn Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr

130 135 140

gtg act tca gcc ctc acc tac cac ctg tgg agg gac agc ctt tgt cca 539

Val Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro

145 150 155

gtg cac cag cct cag ccc acg gag aag agt gac tgaggcccta gggcatggga 592

Val His Gln Pro Gln Pro Thr Glu Lys Ser Asp

160 165 170

gaggagggac gccaggggtg gggaggaaga gtctgcaagc agggctgtgg agttaggggtt 652

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caccccaatg ggaccaccct cctgggtccc ctggtgccgt ttttccttag aaatcagaga 712
aatgggaaaag ggggggaaac tgattttaca cttaaataat aaaatcctat tagtaactct 772
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<210> 20
<211> 170
<212> PRT
<213> Homo sapiens

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Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Leu Cys Glu
          20          25          30
Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu Leu
          35          40          45
Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu Val
          50          55          60
Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro Leu
65          70          75          80
Gly Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val Leu
          85          90          95
Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu Leu
          100         105         110
Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile Asn
          115         120         125
Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr Val
          130         135         140
Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro Val
145         150         155         160
His Gln Pro Gln Thr Glu Lys Ser Asp
          165         170

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<210> 21
<211> 555
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..85

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<220>
<221> CDS
<222> 86..403

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<220>
<221> 3'UTR
<222> 404..555

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<220>
<221> polyA_signal
<222> 504..509

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<220>  
 <221> polyA\_site  
 <222> 540..555

<400> 21

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aaaaacttta cggcaggcgt ccgcgtcgct agctagtcgt tctgaagcgg cggccagaga 60
agagtcaagg gcacgagcat cggcc atg cct ttc ttg gac atc cag aaa agg 112
                               Met Pro Phe Leu Asp Ile Gln Lys Arg
                               1 5
ttc ggc ctt aac ata gat cga tgg ttg aca atc cag agt tgt gaa cag 160
Phe Gly Leu Asn Ile Asp Arg Trp Leu Thr Ile Gln Ser Cys Glu Gln
10 15 20 25
ccc tac aag atg gct ggt cga tgc cat gct ttt gaa aaa gaa tgg ata 208
Pro Tyr Lys Met Ala Gly Arg Cys His Ala Phe Glu Lys Glu Trp Ile
30 35 40
gaa tgt gca cat gga atc ggt tat act cgg gca gag aaa gag tgc aag 256
Glu Cys Ala His Gly Ile Gly Tyr Thr Arg Ala Glu Lys Glu Cys Lys
45 50 55
ata gaa tat gat gat ttc gta gag tgt ttg ctt cgg cag aaa acg atg 304
Ile Glu Tyr Asp Asp Phe Val Glu Cys Leu Leu Arg Gln Lys Thr Met
60 65 70
aga cgt gca ggt acc atc agg aag cag cgg gat aag ctg ata aag gaa 352
Arg Arg Ala Gly Thr Ile Arg Lys Gln Arg Asp Lys Leu Ile Lys Glu
75 80 85
gga aag tac acc cct cca cct cac cac att ggc aag ggg gag cct tgg 400
Gly Lys Tyr Thr Pro Pro Pro His His Ile Gly Lys Gly Glu Pro Trp
90 95 100 105
ccc tgaacagagc agctgctgat gtctggaggc tgattttcct gttctctgtt 453
Pro
ctccactgga aaggttggtt acgacaaacc tccttggtcaa agtgtgtaaa aataaaggat 513
tgctccatcc tatttggttct attttcaaaa aaaaaaaaaa aa 555

```

<210> 22  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

<400> 22

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Met Pro Phe Leu Asp Ile Gln Lys Arg Phe Gly Leu Asn Ile Asp Arg
1 5 10 15
Trp Leu Thr Ile Gln Ser Cys Glu Gln Pro Tyr Lys Met Ala Gly Arg
20 25 30
Cys His Ala Phe Glu Lys Glu Trp Ile Glu Cys Ala His Gly Ile Gly
35 40 45
Tyr Thr Arg Ala Glu Lys Glu Cys Lys Ile Glu Tyr Asp Asp Phe Val
50 55 60
Glu Cys Leu Leu Arg Gln Lys Thr Met Arg Arg Ala Gly Thr Ile Arg
65 70 75 80
Lys Gln Arg Asp Lys Leu Ile Lys Glu Gly Lys Tyr Thr Pro Pro Pro
85 90 95
His His Ile Gly Lys Gly Glu Pro Trp Pro
100 105

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<210> 23

<211> 1726  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..414

<220>  
 <221> CDS  
 <222> 415..1653

<220>  
 <221> 3'UTR  
 <222> 1654..1726

<220>  
 <221> polyA\_site  
 <222> 1688..1726

<400> 23  
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 cgcgtcgggt ggggcgggaa taaagttttt ccaaccagc ttggggagag ggctggatgg 180  
 gaaggaccct ccctgctgca gacttcacgg caggctgcac tgtgtcccct cggctccacg 240  
 gctgccccgg gggcgtgctt ttcgggtttt ctttctagaa tctctggtct gctgctgtgc 300  
 agatggacct gccggcactg ctgtcagaag tgctacgagt ccagctgttg ccagtcaagt 360  
 gaggatgaag ttgaaattct gggacctttc cctgctcaga cccctccctg gctg atg 417  
 Met  
 1  
 gcc agc cgg agc agt gac aag gat ggt gac tct gtc cac acg gcc agc 465  
 Ala Ser Arg Ser Ser Asp Lys Asp Gly Asp Ser Val His Thr Ala Ser  
 5 10 15  
 gaa gtc ccg ctg acc cca cgg acc aat tcc ccg gat gga aga cgc tcg 513  
 Glu Val Pro Leu Thr Pro Arg Thr Asn Ser Pro Asp Gly Arg Arg Ser  
 20 25 30  
 tcc tca gac aca tcc aag tct aca tac agc ctg acg cgg agg att tcg 561  
 Ser Ser Asp Thr Ser Lys Ser Thr Tyr Ser Leu Thr Arg Arg Ile Ser  
 35 40 45  
 agt ctt gag tca aga cgt ccc agc tct cca ctc atc gat att aaa ccc 609  
 Ser Leu Glu Ser Arg Arg Pro Ser Ser Pro Leu Ile Asp Ile Lys Pro  
 50 55 60 65  
 atc gag ttt ggc gtt ctc agc gcc aag aag gag ccc atc caa cct tcg 657  
 Ile Glu Phe Gly Val Leu Ser Ala Lys Lys Glu Pro Ile Gln Pro Ser  
 70 75 80  
 gtg ctc aga cgg acc tat aac ccc gac gac tat ttc agg aag ttc gaa 705  
 Val Leu Arg Arg Thr Tyr Asn Pro Asp Asp Tyr Phe Arg Lys Phe Glu  
 85 90 95  
 ccc cac ctg tac tcc ctc gac tcc aac agc gac gat gtg gac tct ctg 753  
 Pro His Leu Tyr Ser Leu Asp Ser Asn Ser Asp Asp Val Asp Ser Leu  
 100 105 110  
 aca gac gag gag atc ctg tcc aag tac cag ctg ggc atg cag cac ttc 801  
 Thr Asp Glu Glu Ile Leu Ser Lys Tyr Gln Leu Gly Met Gln His Phe  
 115 120 125

agc act cag tac gac ctg ctg cac aac cac ctc acc gtg cgc gtg atc	849
Ser Thr Gln Tyr Asp Leu Leu His Asn His Leu Thr Val Arg Val Ile	
130 135 140 145	
gag gcc agg gac ctg cca cct ccc atc tcc cac gat ggc tcg cgc cag	897
Glu Ala Arg Asp Leu Pro Pro Pro Ile Ser His Asp Gly Ser Arg Gln	
150 155 160	
gac atg gcg cac tcc aac ccc tac gtc aag atc tgt ctc ctg cca gac	945
Asp Met Ala His Ser Asn Pro Tyr Val Lys Ile Cys Leu Leu Pro Asp	
165 170 175	
cag aag aac tca aag cag acc ggg gtc aaa cgc aag acc cag aag ccc	993
Gln Lys Asn Ser Lys Gln Thr Gly Val Lys Arg Lys Thr Gln Lys Pro	
180 185 190	
gtg ttt gag gag cgc tac acc ttc gag atc ccc ttc ctg gag gcc cag	1041
Val Phe Glu Glu Arg Tyr Thr Phe Glu Ile Pro Phe Leu Glu Ala Gln	
195 200 205	
agg agg acc ctg ctc ctg acc gtg gtg gat ttt gat aag ttc tcc cgc	1089
Arg Arg Thr Leu Leu Leu Thr Val Val Asp Phe Asp Lys Phe Ser Arg	
210 215 220 225	
cac tgt gtc att ggg aaa gtt tct gtg cct ttg tgt gaa gtt gac ctg	1137
His Cys Val Ile Gly Lys Val Ser Val Pro Leu Cys Glu Val Asp Leu	
230 235 240	
gtc aag ggc ggg cac tgg tgg aag gcg ctg att ccc agt tct cag aat	1185
Val Lys Gly Gly His Trp Trp Lys Ala Leu Ile Pro Ser Ser Gln Asn	
245 250 255	
gaa gtg gag ctg ggg gag ctg ctt ctg tca ctg aat tat ctc cca agt	1233
Glu Val Glu Leu Gly Glu Leu Leu Leu Ser Leu Asn Tyr Leu Pro Ser	
260 265 270	
gct ggc aga ctg aat gtt gat gtc att cga gcc aag caa ctt ctt cag	1281
Ala Gly Arg Leu Asn Val Asp Val Ile Arg Ala Lys Gln Leu Leu Gln	
275 280 285	
aca gat gtg agc caa ggt tca gac ccc ttt gtg aaa atc cag ctg gtg	1329
Thr Asp Val Ser Gln Gly Ser Asp Pro Phe Val Lys Ile Gln Leu Val	
290 295 300 305	
cat gga ctc aaa ctt gtg aaa acc aag aag acg tcc ttc tta agg ggc	1377
His Gly Leu Lys Leu Val Lys Thr Lys Lys Thr Ser Phe Leu Arg Gly	
310 315 320	
aca att gat cct ttc tac aat gaa tcc ttc agc ttc aaa gtt ccc caa	1425
Thr Ile Asp Pro Phe Tyr Asn Glu Ser Phe Ser Phe Lys Val Pro Gln	
325 330 335	
gaa gaa ctg gaa aat gcc agc cta gtg ttt aca gtt ttc ggc cac aac	1473
Glu Glu Leu Glu Asn Ala Ser Leu Val Phe Thr Val Phe Gly His Asn	
340 345 350	
atg aag agc agc aat gac ttc atc ggg agg atc gtc att ggc cag tac	1521
Met Lys Ser Ser Asn Asp Phe Ile Gly Arg Ile Val Ile Gly Gln Tyr	
355 360 365	
tct tca ggc ccc tct gag acc aac cac tgg agg cgc atg ctc aac acg	1569
Ser Ser Gly Pro Ser Glu Thr Asn His Trp Arg Arg Met Leu Asn Thr	
370 375 380 385	
cac cgc aca gcc gtg gag cag tgg cat agc ctg agg tcc cga gct gag	1617
His Arg Thr Ala Val Glu Gln Trp His Ser Leu Arg Ser Arg Ala Glu	
390 395 400	
tgt gac cgc gtg tct cct gcc tcc ctg gag gtg acc tgagggtgc	1663
Cys Asp Arg Val Ser Pro Ala Ser Leu Glu Val Thr	
405 410	

agggaaggca gcttttcattt gtttaaaaaa aaaaaaaaaa aaagacgaaa aaaaaaaaaa 1723  
 aaa 1726

<210> 24  
 <211> 413  
 <212> PRT  
 <213> Homo sapiens

<400> 24

Met	Ala	Ser	Arg	Ser	Ser	Asp	Lys	Asp	Gly	Asp	Ser	Val	His	Thr	Ala
1				5					10					15	
Ser	Glu	Val	Pro	Leu	Thr	Pro	Arg	Thr	Asn	Ser	Pro	Asp	Gly	Arg	Arg
			20					25					30		
Ser	Ser	Ser	Asp	Thr	Ser	Lys	Ser	Thr	Tyr	Ser	Leu	Thr	Arg	Arg	Ile
		35				40						45			
Ser	Ser	Leu	Glu	Ser	Arg	Arg	Pro	Ser	Ser	Pro	Leu	Ile	Asp	Ile	Lys
	50					55					60				
Pro	Ile	Glu	Phe	Gly	Val	Leu	Ser	Ala	Lys	Lys	Glu	Pro	Ile	Gln	Pro
65					70					75					80
Ser	Val	Leu	Arg	Arg	Thr	Tyr	Asn	Pro	Asp	Asp	Tyr	Phe	Arg	Lys	Phe
				85					90					95	
Glu	Pro	His	Leu	Tyr	Ser	Leu	Asp	Ser	Asn	Ser	Asp	Asp	Val	Asp	Ser
			100					105					110		
Leu	Thr	Asp	Glu	Glu	Ile	Leu	Ser	Lys	Tyr	Gln	Leu	Gly	Met	Gln	His
		115					120					125			
Phe	Ser	Thr	Gln	Tyr	Asp	Leu	Leu	His	Asn	His	Leu	Thr	Val	Arg	Val
	130					135					140				
Ile	Glu	Ala	Arg	Asp	Leu	Pro	Pro	Pro	Ile	Ser	His	Asp	Gly	Ser	Arg
145					150					155					160
Gln	Asp	Met	Ala	His	Ser	Asn	Pro	Tyr	Val	Lys	Ile	Cys	Leu	Leu	Pro
				165				170					175		
Asp	Gln	Lys	Asn	Ser	Lys	Gln	Thr	Gly	Val	Lys	Arg	Lys	Thr	Gln	Lys
		180						185					190		
Pro	Val	Phe	Glu	Glu	Arg	Tyr	Thr	Phe	Glu	Ile	Pro	Phe	Leu	Glu	Ala
		195					200					205			
Gln	Arg	Arg	Thr	Leu	Leu	Leu	Thr	Val	Val	Asp	Phe	Asp	Lys	Phe	Ser
	210					215					220				
Arg	His	Cys	Val	Ile	Gly	Lys	Val	Ser	Val	Pro	Leu	Cys	Glu	Val	Asp
225					230					235					240
Leu	Val	Lys	Gly	Gly	His	Trp	Trp	Lys	Ala	Leu	Ile	Pro	Ser	Ser	Gln
			245						250					255	
Asn	Glu	Val	Glu	Leu	Gly	Glu	Leu	Leu	Leu	Ser	Leu	Asn	Tyr	Leu	Pro
			260					265					270		
Ser	Ala	Gly	Arg	Leu	Asn	Val	Asp	Val	Ile	Arg	Ala	Lys	Gln	Leu	Leu
		275					280					285			
Gln	Thr	Asp	Val	Ser	Gln	Gly	Ser	Asp	Pro	Phe	Val	Lys	Ile	Gln	Leu
	290					295					300				
Val	His	Gly	Leu	Lys	Leu	Val	Lys	Thr	Lys	Lys	Thr	Ser	Phe	Leu	Arg
305					310					315					320
Gly	Thr	Ile	Asp	Pro	Phe	Tyr	Asn	Glu	Ser	Phe	Ser	Phe	Lys	Val	Pro
			325						330					335	
Gln	Glu	Glu	Leu	Glu	Asn	Ala	Ser	Leu	Val	Phe	Thr	Val	Phe	Gly	His
			340					345					350		
Asn	Met	Lys	Ser	Ser	Asn	Asp	Phe	Ile	Gly	Arg	Ile	Val	Ile	Gly	Gln

[illegible]

31

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gtattttcttt aatctaagtt ccatgacatg tgaaaaattc ttttccggtg ggtgtcaccg 469
gaaccggatt  gagaacaggt ttccagatga agctacttgt atgggcttct gcgcaccaaa 529
gaaaattcca tcattttgct acagtccaaa agatggggac tgtgctctgc caatgtgact 589
cgctattatt ttaatccaag atacagaacc tgtgatgctt tcacctatac tggctgtgga 649
gggaatgaca ataactttgt tagcagggag gattgcaaac gtgcatgtgc aaaagctttg 709
aaaaagaaaa agaagatgcc aaagcttcgc tttgccagta gaatccggaa aattcggaag 769
aagcaatttt aaacattctt aatatgtcat cttgtttgtc tttatggctt atttgccttt 829
atggttgtat ctgaagaata atatgacagc atgaggaaac aaatcattgg tgattttattc 889
accagttttt attaatacaa gtcacttttt aaaaataaaa aaaaaaaaaa aa 941

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<210> 26
<211> 88
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..24

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<400> 26
Met Asp Pro Ala Arg Pro Leu Gly Leu Ser Ile Leu Leu Leu Phe Leu
      -20                      -15                      -10
Thr Glu Ala Ala Leu Gly Asp Ala Ala Gln Glu Pro Thr Gly Asn Asn
      -5                      1                      5
Ala Glu Ile Cys Leu Leu Pro Leu Asp Tyr Gly Pro Cys Arg Ala Leu
      10                      15                      20
Leu Leu Arg Tyr Tyr Tyr Asp Arg Tyr Thr Gln Ser Cys Arg Gln Phe
      25                      30                      35                      40
Leu Tyr Gly Gly Cys Glu Gly Asn Ala Asn Asn Phe Tyr Thr Trp Glu
      45                      50                      55
Ala Cys Asp Asp Leu Ala Gly Gly
      60

```

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<210> 27
<211> 1894
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..20

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<220>
<221> CDS
<222> 21..1118

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<220>
<221> 3'UTR
<222> 1119..1894

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<220>
<221> polyA_signal
<222> 1858..1863

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<220>  
 <221> polyA\_site  
 <222> 1879..1894

<400> 27

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agacgtgagc agagcagata atg gca agc atg gct gcc gtg ctc acc tgg gct      53
                Met Ala Ser Met Ala Ala Val Leu Thr Trp Ala
                -20                                -15

ctg gct ctt ctt tca gcg ttt tcg gcc acc cag gca cgg aaa ggc ttc      101
Leu Ala Leu Leu Ser Ala Phe Ser Ala Thr Gln Ala Arg Lys Gly Phe
                -10                                -5                                1

tgg gac tac ttc agc cag acc agc ggg gac aaa ggc agg gtg gag cag      149
Trp Asp Tyr Phe Ser Gln Thr Ser Gly Asp Lys Gly Arg Val Glu Gln
5                10                15                20

atc cat cag cag aag atg gct cgc gag ccc gcg acc ctg aaa gac agc      197
Ile His Gln Gln Lys Met Ala Arg Glu Pro Ala Thr Leu Lys Asp Ser
                25                30                35

ctt gag caa gac ctc aac aat atg aac aag ttc ctg gaa aag ctg agg      245
Leu Glu Gln Asp Leu Asn Asn Met Asn Lys Phe Leu Glu Lys Leu Arg
                40                45                50

cct ctg agt ggg agc gag gct cct cgg ctc cca cag gac ccg gtg ggc      293
Pro Leu Ser Gly Ser Glu Ala Pro Arg Leu Pro Gln Asp Pro Val Gly
                55                60                65

atg cgg cgg cag ctg cag gag gag ttg gag gag gtg aag gct cgc ctc      341
Met Arg Arg Gln Leu Gln Glu Glu Leu Glu Glu Val Lys Ala Arg Leu
70                75                80

cag ccc tac atg gca gag gcg cac gag ctg gtg ggc tgg aat ttg gag      389
Gln Pro Tyr Met Ala Glu Ala His Glu Leu Val Gly Trp Asn Leu Glu
85                90                95                100

ggc ttg cgg cag caa ctg aag ccc tac acg atg gat ctg atg gag cag      437
Gly Leu Arg Gln Gln Leu Lys Pro Tyr Thr Met Asp Leu Met Glu Gln
                105                110                115

gtg gcc ctg cgc gtg cag gag ctg cag gag cag ttg cgc gtg gtg ggg      485
Val Ala Leu Arg Val Gln Glu Leu Gln Glu Gln Leu Arg Val Val Gly
120                125                130

gaa gac acc aag gcc cag ttg ctg ggg ggc gtg gac gag gct tgg gct      533
Glu Asp Thr Lys Ala Gln Leu Leu Gly Gly Val Asp Glu Ala Trp Ala
135                140                145

ttg ctg cag gga ctg cag agc cgc gtg gtg cac cac acc ggc cgc ttc      581
Leu Leu Gln Gly Leu Gln Ser Arg Val Val His His Thr Gly Arg Phe
150                155                160

aaa gag ctc ttc cac cca tac gcc gag agc ctg gtg agc ggc atc ggg      629
Lys Glu Leu Phe His Pro Tyr Ala Glu Ser Leu Val Ser Gly Ile Gly
165                170                175                180

cgc cac gtg cag gag ctg cac cgc agt gtg gct ccg cac gcc ccc gcc      677
Arg His Val Gln Glu Leu His Arg Ser Val Ala Pro His Ala Pro Ala
185                190                195

agc ccc gcg cgc ctc agt cgc tgc gtg cag gtg ctc tcc cgg aag ctc      725
Ser Pro Ala Arg Leu Ser Arg Cys Val Gln Val Leu Ser Arg Lys Leu
200                205                210

acg ctc aag gcc aag gcc ctg cac gca cgc atc cag cag aac ctg gac      773
Thr Leu Lys Ala Lys Ala Leu His Ala Arg Ile Gln Gln Asn Leu Asp
215                220                225

cag ctg cgc gaa gag ctc agc aga gcc ttt gca ggc act ggg act gag      821

```

Gln	Leu	Arg	Glu	Glu	Leu	Ser	Arg	Ala	Phe	Ala	Gly	Thr	Gly	Thr	Glu	
230						235					240					
gaa	ggg	gcc	ggc	ccg	gac	ccc	cag	atg	ctc	tcc	gag	gag	gtg	cgc	cag	869
Glu	Gly	Ala	Gly	Pro	Asp	Pro	Gln	Met	Leu	Ser	Glu	Glu	Val	Arg	Gln	
245					250					255					260	
cga	ctt	cag	gct	ttc	cgc	cag	gac	acc	tac	ctg	cag	ata	gct	gcc	ttc	917
Arg	Leu	Gln	Ala	Phe	Arg	Gln	Asp	Thr	Tyr	Leu	Gln	Ile	Ala	Ala	Phe	
				265					270						275	
act	cgc	gcc	atc	gac	cag	gag	act	gag	gag	gtc	cag	cag	cag	ctg	gcg	965
Thr	Arg	Ala	Ile	Asp	Gln	Glu	Thr	Glu	Glu	Val	Gln	Gln	Gln	Leu	Ala	
			280					285					290			
cca	cct	cca	cca	ggc	cac	agt	gcc	ttc	gcc	cca	gag	ttt	caa	caa	aca	1013
Pro	Pro	Pro	Pro	Gly	His	Ser	Ala	Phe	Ala	Pro	Glu	Phe	Gln	Gln	Thr	
		295					300					305				
gac	agt	ggc	aag	gtt	ctg	agc	aag	ctg	cag	gcc	cgt	ctg	gat	gac	ctg	1061
Asp	Ser	Gly	Lys	Val	Leu	Ser	Lys	Leu	Gln	Ala	Arg	Leu	Asp	Asp	Leu	
	310					315					320					
tgg	gaa	gac	atc	act	cac	agc	ctt	cat	gac	cag	ggc	cac	agc	cat	ctg	1109
Trp	Glu	Asp	Ile	Thr	His	Ser	Leu	His	Asp	Gln	Gly	His	Ser	His	Leu	
	325				330					335					340	
ggg	gac	ccc	tgaggatcta	cctgcccagg	cccattccca	gcttcttgtc										1158
Gly	Asp	Pro														
tggggagcct	tggctctgag	cctctagcat	ggttcagtc	ttgaaaagtg	cctgttgggt											1218
ggaggggtgga	aggctctgtg	caggacaggg	aggccacca	aggggctgct	gtctcctgca											1278
tatccagcct	cctgcgactc	cccaatctgg	atgcattaca	ttcaccaggc	tttgcaaacc											1338
cagcctccca	gtgctcat	gggaatgctc	atgagttact	ccattcaagg	gtgagggagt											1398
agggaggggag	aggcaccatg	catgtgggtg	attatctgca	agcctgtttg	ccgtgatgct											1458
ggaagcctgt	gccactacat	cctggagttt	ggctctagtc	acttctggct	gcctggtggc											1518
caactgtaca	gctggtccac	agagaggagc	acttgtctcc	ccagggctgc	catggcagct											1578
atcaggggaa	tagaaggag	aaagagaata	tcatggggag	aacatgtgat	ggtgtgtgaa											1638
tatccctgct	ggctctgatg	ctgggtgggtg	cgaaagggtg	gggctgtgat	aggagagggc											1698
agagcccatg	tttcttgaca	tagctctaca	cctaaataag	ggactgaacc	ctcccaactg											1758
tgggagctcc	ttaaaccctc	tggggagcat	actgtgtgct	ctccccatct	ccagccctc											1818
cctctgggtt	cccaagttga	agcctagact	tctggctcaa	atgaaataga	tgtttatgat											1878
aaaaaaaaaa	aaaaaaa															1894

<210> 28  
 <211> 366  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..23

<400> 28  
 Met Ala Ser Met Ala Ala Val Leu Thr Trp Ala Leu Ala Leu Leu Ser  
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 Ala Phe Ser Ala Thr Gln Ala Arg Lys Gly Phe Trp Asp Tyr Phe Ser  
           -5                  1                  5  
 Gln Thr Ser Gly Asp Lys Gly Arg Val Glu Gln Ile His Gln Gln Lys  
 10                  15                  20                  25  
 Met Ala Arg Glu Pro Ala Thr Leu Lys Asp Ser Leu Glu Gln Asp Leu  
                   30                  35                  40

Asn	Asn	Met	Asn	Lys	Phe	Leu	Glu	Lys	Leu	Arg	Pro	Leu	Ser	Gly	Ser		
			45					50					55				
Glu	Ala	Pro	Arg	Leu	Pro	Gln	Asp	Pro	Val	Gly	Met	Arg	Arg	Gln	Leu		
		60					65					70					
Gln	Glu	Glu	Leu	Glu	Glu	Val	Lys	Ala	Arg	Leu	Gln	Pro	Tyr	Met	Ala		
		75				80					85						
Glu	Ala	His	Glu	Leu	Val	Gly	Trp	Asn	Leu	Glu	Gly	Leu	Arg	Gln	Gln		
90					95					100					105		
Leu	Lys	Pro	Tyr	Thr	Met	Asp	Leu	Met	Glu	Gln	Val	Ala	Leu	Arg	Val		
				110					115					120			
Gln	Glu	Leu	Gln	Glu	Gln	Leu	Arg	Val	Val	Gly	Glu	Asp	Thr	Lys	Ala		
			125					130					135				
Gln	Leu	Leu	Gly	Gly	Val	Asp	Glu	Ala	Trp	Ala	Leu	Leu	Gln	Gly	Leu		
		140					145					150					
Gln	Ser	Arg	Val	Val	His	His	Thr	Gly	Arg	Phe	Lys	Glu	Leu	Phe	His		
	155					160					165						
Pro	Tyr	Ala	Glu	Ser	Leu	Val	Ser	Gly	Ile	Gly	Arg	His	Val	Gln	Glu		
170					175					180					185		
Leu	His	Arg	Ser	Val	Ala	Pro	His	Ala	Pro	Ala	Ser	Pro	Ala	Arg	Leu		
				190					195					200			
Ser	Arg	Cys	Val	Gln	Val	Leu	Ser	Arg	Lys	Leu	Thr	Leu	Lys	Ala	Lys		
		205						210					215				
Ala	Leu	His	Ala	Arg	Ile	Gln	Gln	Asn	Leu	Asp	Gln	Leu	Arg	Glu	Glu		
		220					225					230					
Leu	Ser	Arg	Ala	Phe	Ala	Gly	Thr	Gly	Thr	Glu	Glu	Gly	Ala	Gly	Pro		
	235					240					245						
Asp	Pro	Gln	Met	Leu	Ser	Glu	Glu	Val	Arg	Gln	Arg	Leu	Gln	Ala	Phe		
250					255					260					265		
Arg	Gln	Asp	Thr	Tyr	Leu	Gln	Ile	Ala	Ala	Phe	Thr	Arg	Ala	Ile	Asp		
			270						275					280			
Gln	Glu	Thr	Glu	Glu	Val	Gln	Gln	Gln	Leu	Ala	Pro	Pro	Pro	Pro	Gly		
		285						290					295				
His	Ser	Ala	Phe	Ala	Pro	Glu	Phe	Gln	Gln	Thr	Asp	Ser	Gly	Lys	Val		
		300					305					310					
Leu	Ser	Lys	Leu	Gln	Ala	Arg	Leu	Asp	Asp	Leu	Trp	Glu	Asp	Ile	Thr		
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His	Ser	Leu	His	Asp	Gln	Gly	His	Ser	His	Leu	Gly	Asp	Pro				
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<222> 560..742

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<222> 728..742

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cct agt aca gac tca gga aaa gaa gaa tat att gcc acg ttc aaa gga      100
Pro Ser Thr Asp Ser Gly Lys Glu Tyr Ile Ala Thr Phe Lys Gly
      10           15           20
tct gaa tac ttc tgc tac gac ttg tct caa aac ccc att caa agc agc      148
Ser Glu Tyr Phe Cys Tyr Asp Leu Ser Gln Asn Pro Ile Gln Ser Ser
      25           30           35
agt gat gaa ata act ctg tca ttt aaa acc ctt cag agg aat gga ctg      196
Ser Asp Glu Ile Thr Leu Ser Phe Lys Thr Leu Gln Arg Asn Gly Leu
      40           45           50           55
atg ctt cac act ggg aaa tcg gct gat tat gtc aat ctt gcc ctg aaa      244
Met Leu His Thr Gly Lys Ser Ala Asp Tyr Val Asn Leu Ala Leu Lys
      60           65           70
aat gga gct gtc tct ctg gtc att aat ttg gga tca ggg gcc ttt gaa      292
Asn Gly Ala Val Ser Leu Val Ile Asn Leu Gly Ser Gly Ala Phe Glu
      75           80           85
gca cta gtg gag cct gtg aat gga aag ttt aat gat aat gcc tgg cat      340
Ala Leu Val Glu Pro Val Asn Gly Lys Phe Asn Asp Asn Ala Trp His
      90           95           100
gat gtg aaa gtc acc agg aat ctg cgt cag gtg aca ata tca gtg gat      388
Asp Val Lys Val Thr Arg Asn Leu Arg Gln Val Thr Ile Ser Val Asp
      105          110          115
ggg att ctt acc aca acg ggc tac acg caa gaa gat tat acc atg ctg      436
Gly Ile Leu Thr Thr Gly Tyr Thr Gln Glu Asp Tyr Thr Met Leu
      120          125          130          135
ggg tct gat gac ttt ttc tat gtt gga ggc agt ccc agc aca gcc gac      484
Gly Ser Asp Asp Phe Phe Tyr Val Gly Gly Ser Pro Ser Thr Ala Asp
      140          145          150
ctt cca ggg tca cca atc cag cat gaa agc acc ttt gct gaa gac ccg      532
Leu Pro Gly Ser Pro Ile Gln His Glu Ser Thr Phe Ala Glu Asp Pro
      155          160          165
atg ttc cag agt caa acg gca caa ctt taaattcaat attctactat      579
Met Phe Gln Ser Gln Thr Ala Gln Leu
      170          175
tgtttatgta ggattggggg agggaaacag ctcatagatc attatgaagg aattagggttc 639
ctcttcttta ttagtctgta agtaatttac atttgagatt tgtgtggaca gttgatatta 699
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<213> Homo sapiens

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Tyr	Ile	Ala	Thr	Phe	Lys	Gly	Ser	Glu	Tyr	Phe	Cys	Tyr	Asp	Leu	Ser
			20					25					30		
Gln	Asn	Pro	Ile	Gln	Ser	Ser	Ser	Asp	Glu	Ile	Thr	Leu	Ser	Phe	Lys
		35					40					45			
Thr	Leu	Gln	Arg	Asn	Gly	Leu	Met	Leu	His	Thr	Gly	Lys	Ser	Ala	Asp
	50				55						60				
Tyr	Val	Asn	Leu	Ala	Leu	Lys	Asn	Gly	Ala	Val	Ser	Leu	Val	Ile	Asn
65					70				75					80	
Leu	Gly	Ser	Gly	Ala	Phe	Glu	Ala	Leu	Val	Glu	Pro	Val	Asn	Gly	Lys
			85						90					95	
Phe	Asn	Asp	Asn	Ala	Trp	His	Asp	Val	Lys	Val	Thr	Arg	Asn	Leu	Arg
			100					105					110		
Gln	Val	Thr	Ile	Ser	Val	Asp	Gly	Ile	Leu	Thr	Thr	Thr	Gly	Tyr	Thr
		115					120						125		
Gln	Glu	Asp	Tyr	Thr	Met	Leu	Gly	Ser	Asp	Asp	Phe	Phe	Tyr	Val	Gly
	130					135					140				
Gly	Ser	Pro	Ser	Thr	Ala	Asp	Leu	Pro	Gly	Ser	Pro	Ile	Gln	His	Glu
145					150					155				160	
Ser	Thr	Phe	Ala	Glu	Asp	Pro	Met	Phe	Gln	Ser	Gln	Thr	Ala	Gln	Leu
				165					170					175	

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48

1	5	10	15	
cga gtc tcc gac ctt cag atg ctc ctg ggt ttc gtg ggc cgg agt aag				96
Arg Val Ser Asp Leu Gln Met Leu Leu Gly Phe Val Gly Arg Ser Lys				
20	25	30		
agt gga ctg aag cac gag ctc gtc acc agg gcc ctc cag ctg gtg cag				144
Ser Gly Leu Lys His Glu Leu Val Thr Arg Ala Leu Gln Leu Val Gln				
35	40	45		
ttt gac tgt acc cct gag ctg ttc aag aag atc aag gag ctg tac gag				192
Phe Asp Cys Thr Pro Glu Leu Phe Lys Lys Ile Lys Glu Leu Tyr Glu				
50	55	60		
acc cgc tac gcc aag aag aac tcg gag cct gcc cca cag ccg cac cgg				240
Thr Arg Tyr Ala Lys Lys Asn Ser Glu Pro Ala Pro Gln Pro His Arg				
65	70	75		
ccc ctg gac ccc ctg acc atg cac tcc acc tac gac cgg gcc ggc gct				288
Pro Leu Asp Pro Leu Thr Met His Ser Thr Tyr Asp Arg Ala Gly Ala				
80	85	90	95	
gtg ccc agg act ccg ctg gca ggc ccc aat att gac tac ccc gtg ctc				336
Val Pro Arg Thr Pro Leu Ala Gly Pro Asn Ile Asp Tyr Pro Val Leu				
100	105	110		
tac gga aag tac tta aac gga ctg gga ttg ccc gcc aag acc ctc				384
Tyr Gly Lys Tyr Leu Asn Gly Leu Gly Arg Leu Pro Ala Lys Thr Leu				
115	120	125		
aag cca gaa gtc cgc ctg gtg aag ctg ccg ttc ttt aat atg ctg gac				432
Lys Pro Glu Val Arg Leu Val Lys Leu Pro Phe Phe Asn Met Leu Asp				
130	135	140		
gag ctg ctg aag ccc acc gaa tta gtc cca cag aac aac gag aag ctt				480
Glu Leu Leu Lys Pro Thr Glu Leu Val Pro Gln Asn Asn Glu Lys Leu				
145	150	155		
cag gag agc ccg tgc atc ttc gca ttg acg cca aga cag gtg gag ttg				528
Gln Glu Ser Pro Cys Ile Phe Ala Leu Thr Pro Arg Gln Val Glu Leu				
160	165	170	175	
atc cgg aac tcc agg gaa ctg cag ccc gga gtt aaa gcc gtg cag gtc				576
Ile Arg Asn Ser Arg Glu Leu Gln Pro Gly Val Lys Ala Val Gln Val				
180	185	190		
gtc ctg aga atc tgt tac tca gac acc agc tgc cct cag gag gac cag				624
Val Leu Arg Ile Cys Tyr Ser Asp Thr Ser Cys Pro Gln Glu Asp Gln				
195	200	205		
tac ccg ccc aac atc gct gtg aag gtc aac cac agc tac tgc tcc gtc				672
Tyr Pro Pro Asn Ile Ala Val Lys Val Asn His Ser Tyr Cys Ser Val				
210	215	220		
ccg ggc tac tac ccc tcc aat aag ccc ggg gtg gag ccc aag agg ccg				720
Pro Gly Tyr Tyr Pro Ser Asn Lys Pro Gly Val Glu Pro Lys Arg Pro				
225	230	235		
tgc cgc ccc atc aac ctc acc cac ctc atg tac ctt tcc tcg gcc acc				768
Cys Arg Pro Ile Asn Leu Thr His Leu Met Tyr Leu Ser Ser Ala Thr				
240	245	250	255	
aac cgc atc act gtc acc tgg ggg aac tac ggc aag agc tac tcg gtg				816
Asn Arg Ile Thr Val Thr Trp Gly Asn Tyr Gly Lys Ser Tyr Ser Val				
260	265	270		
gcc ctg tac ctg gtg cgg cag ctg acc tca tcg gag ctg ctg cag agg				864
Ala Leu Tyr Leu Val Arg Gln Leu Thr Ser Ser Glu Leu Leu Gln Arg				
275	280	285		
ctg aag acc att ggg gta aag cac ccg gag ctg tgc aag gca ctg gtc				912
Leu Lys Thr Ile Gly Val Lys His Pro Glu Leu Cys Lys Ala Leu Val				

290	295	300	
aag gag aag ctg cgc ctt gat cct gac agc gag atc gcc acc acc ggt			960
Lys Glu Lys Leu Arg Leu Asp Pro Asp Ser Glu Ile Ala Thr Thr Gly			
305	310	315	
gtg cgg gtg tcc ctc atc tgt ccg ctg gtg aag atg cgg ctc tcc gtg			1008
Val Arg Val Ser Leu Ile Cys Pro Leu Val Lys Met Arg Leu Ser Val			
320	325	330	335
ccc tgc cgg gca gag acc tgc gcc cac ctg cag tgc ttc gac gcc gtc			1056
Pro Cys Arg Ala Glu Thr Cys Ala His Leu Gln Cys Phe Asp Ala Val			
340	345	350	
ttc tac ctg cag atg aac gag aag aag ccc acc tgg atg tgc ccc gtg			1104
Phe Tyr Leu Gln Met Asn Glu Lys Lys Pro Thr Trp Met Cys Pro Val			
355	360	365	
tgc gac aag cca gcc ccc tac gac cag ctc atc atc gac ggg ctc ctc			1152
Cys Asp Lys Pro Ala Pro Tyr Asp Gln Leu Ile Ile Asp Gly Leu Leu			
370	375	380	
tcg aag atc ctg agc gag tgt gag gac gcc gac gag atc gag tac ctg			1200
Ser Lys Ile Leu Ser Glu Cys Glu Asp Ala Asp Glu Ile Glu Tyr Leu			
385	390	395	
gtg gac ggc tcg tgg tgc ccg atc cgc gcc gaa aag gag ctc agc tgc			1248
Val Asp Gly Ser Trp Cys Pro Ile Arg Ala Glu Lys Glu Leu Ser Cys			
400	405	410	415
agc ccg cag ggc gcc atc ctc gtg ctg ggc ccc tcg gac gcc aat ggg			1296
Ser Pro Gln Gly Ala Ile Leu Val Leu Gly Pro Ser Asp Ala Asn Gly			
420	425	430	
ctc ctg ccc gcc ccc agc gtc aac ggg agc ggt gcc ctg ggc agc acg			1344
Leu Leu Pro Ala Pro Ser Val Asn Gly Ser Gly Ala Leu Gly Ser Thr			
435	440	445	
ggg ggc ggc ggc ccg gtg ggc agc atg gag aat ggg aag ccg ggc gcc			1392
Gly Gly Gly Gly Pro Val Gly Ser Met Glu Asn Gly Lys Pro Gly Ala			
450	455	460	
gat gtg gtg gac ctc acg ctg gac agc tca tcg tcc tcg gag gat gag			1440
Asp Val Val Asp Leu Thr Leu Asp Ser Ser Ser Ser Ser Glu Asp Glu			
465	470	475	
gag gag gag gaa gag gag gag gaa gac gag gac gaa gag ggg ccc cgg			1488
Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Glu Gly Pro Arg			
480	485	490	495
ccc aag cgc cgc tgc ccc ttc cag aag ggc ctg gtg ccg gcc tgc			1533
Pro Lys Arg Arg Cys Pro Phe Gln Lys Gly Leu Val Pro Ala Cys			
500	505	510	
tgaccccgcc cgcacacttg acttttcctgg tgctcaccac gcagaggggc acggggccagc			1593
ctcggggcgca gagggaggag tgacctttct ttttcctttt attgtcgttc gttttgtttt			1653
tccacccttt tgctggctc ctggcacctg tacctctgga ctctcctatc gggggattaa			1713
aaaaaaaaagt aaaatgacaa aaaaagatac aaaaaagaaa aaaaaaaaaa aaa			1766

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 <212> PRT  
 <213> Homo sapiens

<400> 32  
 Met Ala Ala Glu Leu Val Glu Ala Lys Asn Met Val Met Ser Phe Arg  
 1 5 10 15  
 Val Ser Asp Leu Gln Met Leu Leu Gly Phe Val Gly Arg Ser Lys Ser





450		455		460
Val Val Asp Leu Thr Leu Asp Ser Ser Ser Ser Ser Glu Asp Glu Glu				
465		470		475
Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Glu Gly Pro Arg Pro				
	485		490	495
Lys Arg Arg Cys Pro Phe Gln Lys Gly Leu Val Pro Ala Cys				
500		505		510

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 Met Leu Leu Leu Ser Leu Thr Leu Ser Leu Val Leu Leu  
 -15 -10  
 ggc tcc tcc tgg ggc tgc ggc att cct gcc atc aaa ccg gca ctg agc 97  
 Gly Ser Ser Trp Gly Cys Gly Ile Pro Ala Ile Lys Pro Ala Leu Ser  
 -5 1 5 10  
 ttc agc cag agg att gtc aac ggg gag aat gca gtg ttg ggc tcc tgg 145  
 Phe Ser Gln Arg Ile Val Asn Gly Glu Asn Ala Val Leu Gly Ser Trp  
 15 20 25  
 ccc tgg cag gtg tcc ctg cag gac agc agc gac ttc cac ttc tgc ggt 193  
 Pro Trp Gln Val Ser Leu Gln Asp Ser Ser Asp Phe His Phe Cys Gly  
 30 35 40  
 ggt tct ctc atc agc cag tcc tgg gtg gtc act gct gcc cac tgc aat 241  
 Gly Ser Leu Ile Ser Gln Ser Trp Val Val Thr Ala Ala His Cys Asn  
 45 50 55  
 gtc agc cct ggc cgc cat ttt gtt gtc ctg ggc gag tat gac cga tca 289  
 Val Ser Pro Gly Arg His Phe Val Val Leu Gly Glu Tyr Asp Arg Ser  
 60 65 70 75  
 tca aac gca gag ccc ttg cag gtt ctg tcc gtc tct cgg gcc att aca 337  
 Ser Asn Ala Glu Pro Leu Gln Val Leu Ser Val Ser Arg Ala Ile Thr

				80					85				90				
cac	cct	agc	tgg	aac	tct	acc	acc	atg	aac	aat	gac	gtg	acg	ctg	ctg		385
His	Pro	Ser	Trp	Asn	Ser	Thr	Thr	Met	Asn	Asn	Asp	Val	Thr	Leu	Leu		
				95				100					105				
aag	ctc	gcc	tcg	cca	gcc	cag	tac	aca	aca	cgc	atc	tcg	cca	ggt	tgc		433
Lys	Leu	Ala	Ser	Pro	Ala	Gln	Tyr	Thr	Thr	Arg	Ile	Ser	Pro	Val	Cys		
				110				115					120				
ctg	gca	tcc	tca	aac	gag	gct	ctg	act	gaa	ggc	ctc	acg	tgt	gtc	acc		481
Leu	Ala	Ser	Ser	Asn	Glu	Ala	Leu	Thr	Glu	Gly	Leu	Thr	Cys	Val	Thr		
				125				130					135				
acc	ggc	tgg	ggg	cgc	ctc	agt	ggc	gtg	ggc	aat	gtg	aca	cca	gca	cgt		529
Thr	Gly	Trp	Gly	Arg	Leu	Ser	Gly	Val	Gly	Asn	Val	Thr	Pro	Ala	Arg		
				140				145					150				
ctg	cag	cag	gtg	gct	ttg	ccc	ctg	gtc	act	gtg	aat	cag	tgc	cgg	cag		577
Leu	Gln	Gln	Val	Ala	Leu	Pro	Leu	Val	Thr	Val	Asn	Gln	Cys	Arg	Gln		
				160				165					170				
tac	tgg	ggc	tca	agt	atc	act	gac	tcc	atg	atc	tgt	gca	ggg	ggc	gca		625
Tyr	Trp	Gly	Ser	Ser	Ile	Thr	Asp	Ser	Met	Ile	Cys	Ala	Gly	Gly	Ala		
				175				180					185				
ggg	gcc	tcc	tcg	tgc	cag	ggg	gac	tcc	gga	ggc	cct	ctt	gtc	tgc	cag		673
Gly	Ala	Ser	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Gln		
				190				195					200				
aag	gga	aac	aca	tgg	gtg	ctt	att	ggg	att	gtc	tcc	tgg	ggc	acc	aaa		721
Lys	Gly	Asn	Thr	Trp	Val	Leu	Ile	Gly	Ile	Val	Ser	Trp	Gly	Thr	Lys		
				205				210					215				
aac	tgc	aat	gtg	cgc	gca	cct	gct	gtg	tat	act	cga	ggt	agc	aag	ttc		769
Asn	Cys	Asn	Val	Arg	Ala	Pro	Ala	Val	Tyr	Thr	Arg	Val	Ser	Lys	Phe		
				220				225					230				
agc	acc	tgg	atc	aac	cag	gtc	ata	gcc	tac	aac	tgagctcacc	acaggccctc					822
Ser	Thr	Trp	Ile	Asn	Gln	Val	Ile	Ala	Tyr	Asn							
				240				245									
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<213> Homo sapiens

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<221> SIGNAL

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<400> 34

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				1			5				10						
Arg	Ile	Val	Asn	Gly	Glu	Asn	Ala	Val	Leu	Gly	Ser	Trp	Pro	Trp	Gln		
				15			20				25				30		
Val	Ser	Leu	Gln	Asp	Ser	Ser	Asp	Phe	His	Phe	Cys	Gly	Gly	Ser	Leu		
				35				40						45			
Ile	Ser	Gln	Ser	Trp	Val	Val	Thr	Ala	Ala	His	Cys	Asn	Val	Ser	Pro		
				50			55					60					
Gly	Arg	His	Phe	Val	Val	Leu	Gly	Glu	Tyr	Asp	Arg	Ser	Ser	Asn	Ala		

	65					70					75				
Glu	Pro	Leu	Gln	Val	Leu	Ser	Val	Ser	Arg	Ala	Ile	Thr	His	Pro	Ser
	80					85					90				
Trp	Asn	Ser	Thr	Thr	Met	Asn	Asn	Asp	Val	Thr	Leu	Leu	Lys	Leu	Ala
95					100					105					110
Ser	Pro	Ala	Gln	Tyr	Thr	Thr	Arg	Ile	Ser	Pro	Val	Cys	Leu	Ala	Ser
			115						120					125	
Ser	Asn	Glu	Ala	Leu	Thr	Glu	Gly	Leu	Thr	Cys	Val	Thr	Thr	Gly	Trp
		130					135						140		
Gly	Arg	Leu	Ser	Gly	Val	Gly	Asn	Val	Thr	Pro	Ala	Arg	Leu	Gln	Gln
	145						150					155			
Val	Ala	Leu	Pro	Leu	Val	Thr	Val	Asn	Gln	Cys	Arg	Gln	Tyr	Trp	Gly
	160					165					170				
Ser	Ser	Ile	Thr	Asp	Ser	Met	Ile	Cys	Ala	Gly	Gly	Ala	Gly	Ala	Ser
175					180					185					190
Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Gln	Lys	Gly	Asn
			195						200					205	
Thr	Trp	Val	Leu	Ile	Gly	Ile	Val	Ser	Trp	Gly	Thr	Lys	Asn	Cys	Asn
		210						215					220		
Val	Arg	Ala	Pro	Ala	Val	Tyr	Thr	Arg	Val	Ser	Lys	Phe	Ser	Thr	Trp
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Ile	Asn	Gln	Val	Ile	Ala	Tyr	Asn								
	240					245									

<210> 35  
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 Met Ile Pro Thr Phe Thr  
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 gct ctg ctc tgc ctc ggg ctg agt ctg ggc ccc agg acc cac atg cag 103  
 Ala Leu Leu Cys Leu Gly Leu Ser Leu Gly Pro Arg Thr His Met Gln  
 -15 -10 -5  
 gca ggg ccc ctc ccc aaa ccc acc ctc tgg gct gag cca ggc tct gtg 151  
 Ala Gly Pro Leu Pro Lys Pro Thr Leu Trp Ala Glu Pro Gly Ser Val

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atc agc tgg ggg aac tct gtg acc atc tgg tgt cag ggg acc ctg gag				199
Ile Ser Trp Gly Asn Ser Val Thr Ile Trp Cys Gln Gly Thr Leu Glu				
20	25	30		
gct cgg gag tac cgt ctg gat aaa gag gaa agc cca gca ccc tgg gac				247
Ala Arg Glu Tyr Arg Leu Asp Lys Glu Glu Ser Pro Ala Pro Trp Asp				
35	40	45		
aga cag aac cca ctg gag ccc aag aac aag gcc aga ttc tcc atc cca				295
Arg Gln Asn Pro Leu Glu Pro Lys Asn Lys Ala Arg Phe Ser Ile Pro				
50	55	60		
tcc atg aca gag gac tat gca ggg aga tac cgc tgt tac tat cgc agc				343
Ser Met Thr Glu Asp Tyr Ala Gly Arg Tyr Arg Cys Tyr Tyr Arg Ser				
65	70	75		
cct gta ggc tgg tca cag ccc agt gac ccc ctg gag ctg gtg atg aca				391
Pro Val Gly Trp Ser Gln Pro Ser Asp Pro Leu Glu Leu Val Met Thr				
80	85	90		
gga gcc tac agt aaa ccc acc ctt tca gcc ctg ccg agt cct ctt gtg				439
Gly Ala Tyr Ser Lys Pro Thr Leu Ser Ala Leu Pro Ser Pro Leu Val				
100	105	110		
acc tca gaa aag agc gtg acc ctg ctg tgt cag tca cgg agc cca atg				487
Thr Ser Glu Lys Ser Val Thr Leu Leu Cys Gln Ser Arg Ser Pro Met				
115	120	125		
gac act ttc ctt ctg atc aag gag cgg gca gcc cat ccc cta ctg cat				535
Asp Thr Phe Leu Leu Ile Lys Glu Arg Ala Ala His Pro Leu Leu His				
130	135	140		
ctg aga tca gag cac gga gct cag cag cac cag gct gaa ttc ccc atg				583
Leu Arg Ser Glu His Gly Ala Gln Gln His Gln Ala Glu Phe Pro Met				
145	150	155		
agt cct gtg acc tca gtg cac ggg ggg acc tac agg tgc ttc agc tca				631
Ser Pro Val Thr Ser Val His Gly Gly Thr Tyr Arg Cys Phe Ser Ser				
160	165	170		
cac ggc ttc tcc cac tac ctg ctg tca cac ccc agt gac ccc ctg gag				679
His Gly Phe Ser His Tyr Leu Leu Ser His Pro Ser Asp Pro Leu Glu				
180	185	190		
ctc ata gtc tca gga tcc ttg gag gat ccc agg ccc tca ccc aca agg				727
Leu Ile Val Ser Gly Ser Leu Glu Asp Pro Arg Pro Ser Pro Thr Arg				
195	200	205		
tcc gtc tca aca gct gca ggc cct gag gac cag ccc ctc atg cct aca				775
Ser Val Ser Thr Ala Ala Gly Pro Glu Asp Gln Pro Leu Met Pro Thr				
210	215	220		
ggg tca gtc ccc cac agt ggt ctg aga agg cac tgg gag gta ctg atc				823
Gly Ser Val Pro His Ser Gly Leu Arg Arg His Trp Glu Val Leu Ile				
225	230	235		
ggg gtc ttg gtg gtc tcc atc ctg ctt ctc tcc ctc ctc ctc ttc ctc				871
Gly Val Leu Val Val Ser Ile Leu Leu Leu Ser Leu Leu Leu Phe Leu				
240	245	250		
ctc ctc caa cac tgg cgt cag gga aaa cac agg aca ttg gcc cag aga				919
Leu Leu Gln His Trp Arg Gln Gly Lys His Arg Thr Leu Ala Gln Arg				
260	265	270		
cag gct gat ttc caa cgt cct cca ggg gct gcc gag cca gag ccc aag				967
Gln Ala Asp Phe Gln Arg Pro Pro Ala Ala Glu Pro Glu Pro Lys				
275	280	285		
gac ggg ggc cta cag agg agg tcc agc cca gct gct gac gtc cag gga				1015
Asp Gly Gly Leu Gln Arg Arg Ser Ser Pro Ala Ala Asp Val Gln Gly				

290	295	300	
gaa aac ttc tgt gct gcc gtg aag gac aca cag cct gag gac ggg gtg			1063
Glu Asn Phe Cys Ala Ala Val Lys Asp Thr Gln Pro Glu Asp Gly Val			
305	310	315	
gaa atg gac act cgg agc cca cac gat gaa gac ccc cag gca gtg acg			1111
Glu Met Asp Thr Arg Ser Pro His Asp Glu Asp Pro Gln Ala Val Thr			
320	325	330	335
tat gcc aag gtg aaa cac tcc aga cct agg aga gaa atg gcc tct cct			1159
Tyr Ala Lys Val Lys His Ser Arg Pro Arg Arg Glu Met Ala Ser Pro			
340	345	350	
ccc tcc cca ctg tct ggg gaa ttc ctg gac aca aag gac aga cag gca			1207
Pro Ser Pro Leu Ser Gly Glu Phe Leu Asp Thr Lys Asp Arg Gln Ala			
355	360	365	
gaa gag gac aga cag atg gac act gag gct gct gca tct gaa gcc ccc			1255
Glu Glu Asp Arg Gln Met Asp Thr Glu Ala Ala Ala Ser Glu Ala Pro			
370	375	380	
cag gat gtg acc tac gcc cag ctg cac agc ttt acc ctc aga cag aag			1303
Gln Asp Val Thr Tyr Ala Gln Leu His Ser Phe Thr Leu Arg Gln Lys			
385	390	395	
gca act gag cct cct cca tcc cag gaa ggg gcc tct cca gct gag ccc			1351
Ala Thr Glu Pro Pro Ser Gln Glu Gly Ala Ser Pro Ala Glu Pro			
400	405	410	415
agt gtc tat gcc act ctg gcc atc cac taatccaggg gggacccaga			1398
Ser Val Tyr Ala Thr Leu Ala Ile His			
420			
ccccacaagc catggagact caggacccca gaaggcatgg aagctgcctc cagtagacat			1458
cactgaaccc cagccagccc agaccctga cacagaccac tagaagattc cgggaacgtt			1518
gggagtcacc tgattctgca aagataaata atatccctgc attatcaaaa taaagtagca			1578
gacctctcaa ttcacaatga gttaactgat aaaacaaaac agaagtcaga caatgtttta			1638
aattgaatga tcatgtaaatt attacacatc aaaccaatga catgggaaaa tgggagcttc			1698
taatgaggac aaacaaaaaa aaaaaaaaaa			1728

<210> 36  
 <211> 447  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..23

<400> 36  
 Met Ile Pro Thr Phe Thr Ala Leu Leu Cys Leu Gly Leu Ser Leu Gly  
                   -20                  -15                  -10  
 Pro Arg Thr His Met Gln Ala Gly Pro Leu Pro Lys Pro Thr Leu Trp  
                   -5                  1                  5  
 Ala Glu Pro Gly Ser Val Ile Ser Trp Gly Asn Ser Val Thr Ile Trp  
 10                  15                  20                  25  
 Cys Gln Gly Thr Leu Glu Ala Arg Glu Tyr Arg Leu Asp Lys Glu Glu  
                   30                  35                  40  
 Ser Pro Ala Pro Trp Asp Arg Gln Asn Pro Leu Glu Pro Lys Asn Lys  
                   45                  50                  55  
 Ala Arg Phe Ser Ile Pro Ser Met Thr Glu Asp Tyr Ala Gly Arg Tyr  
                   60                  65                  70

Arg	Cys	Tyr	Tyr	Arg	Ser	Pro	Val	Gly	Trp	Ser	Gln	Pro	Ser	Asp	Pro
75						80					85				
Leu	Glu	Leu	Val	Met	Thr	Gly	Ala	Tyr	Ser	Lys	Pro	Thr	Leu	Ser	Ala
90					95					100					105
Leu	Pro	Ser	Pro	Leu	Val	Thr	Ser	Glu	Lys	Ser	Val	Thr	Leu	Leu	Cys
				110					115						120
Gln	Ser	Arg	Ser	Pro	Met	Asp	Thr	Phe	Leu	Leu	Ile	Lys	Glu	Arg	Ala
			125					130					135		
Ala	His	Pro	Leu	Leu	His	Leu	Arg	Ser	Glu	His	Gly	Ala	Gln	Gln	His
		140					145					150			
Gln	Ala	Glu	Phe	Pro	Met	Ser	Pro	Val	Thr	Ser	Val	His	Gly	Gly	Thr
	155				160						165				
Tyr	Arg	Cys	Phe	Ser	Ser	His	Gly	Phe	Ser	His	Tyr	Leu	Leu	Ser	His
170					175					180					185
Pro	Ser	Asp	Pro	Leu	Glu	Leu	Ile	Val	Ser	Gly	Ser	Leu	Glu	Asp	Pro
				190					195					200	
Arg	Pro	Ser	Pro	Thr	Arg	Ser	Val	Ser	Thr	Ala	Ala	Gly	Pro	Glu	Asp
			205					210					215		
Gln	Pro	Leu	Met	Pro	Thr	Gly	Ser	Val	Pro	His	Ser	Gly	Leu	Arg	Arg
		220					225					230			
His	Trp	Glu	Val	Leu	Ile	Gly	Val	Leu	Val	Val	Ser	Ile	Leu	Leu	Leu
	235					240					245				
Ser	Leu	Leu	Leu	Phe	Leu	Leu	Leu	Gln	His	Trp	Arg	Gln	Gly	Lys	His
250					255					260					265
Arg	Thr	Leu	Ala	Gln	Arg	Gln	Ala	Asp	Phe	Gln	Arg	Pro	Pro	Gly	Ala
			270						275					280	
Ala	Glu	Pro	Glu	Pro	Lys	Asp	Gly	Gly	Leu	Gln	Arg	Arg	Ser	Ser	Pro
			285					290					295		
Ala	Ala	Asp	Val	Gln	Gly	Glu	Asn	Phe	Cys	Ala	Ala	Val	Lys	Asp	Thr
		300					305					310			
Gln	Pro	Glu	Asp	Gly	Val	Glu	Met	Asp	Thr	Arg	Ser	Pro	His	Asp	Glu
	315					320					325				
Asp	Pro	Gln	Ala	Val	Thr	Tyr	Ala	Lys	Val	Lys	His	Ser	Arg	Pro	Arg
330					335					340					345
Arg	Glu	Met	Ala	Ser	Pro	Pro	Ser	Pro	Leu	Ser	Gly	Glu	Phe	Leu	Asp
				350					355					360	
Thr	Lys	Asp	Arg	Gln	Ala	Glu	Glu	Asp	Arg	Gln	Met	Asp	Thr	Glu	Ala
			365					370					375		
Ala	Ala	Ser	Glu	Ala	Pro	Gln	Asp	Val	Thr	Tyr	Ala	Gln	Leu	His	Ser
		380					385					390			
Phe	Thr	Leu	Arg	Gln	Lys	Ala	Thr	Glu	Pro	Pro	Pro	Ser	Gln	Glu	Gly
	395					400					405				
Ala	Ser	Pro	Ala	Glu	Pro	Ser	Val	Tyr	Ala	Thr	Leu	Ala	Ile	His	
410					415					420					

<210> 37  
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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 1..329

<220>  
 <221> CDS  
 <222> 330..1478

<220>  
 <221> 3'UTR  
 <222> 1479..1757

<220>  
 <221> polyA\_signal  
 <222> 1722..1727

<220>  
 <221> polyA\_site  
 <222> 1742..1757

<400> 37  
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 gctcgagggg caagggggct cgggtgtgtt acaccaggca cgggctacga gcgtccatcc 120  
 cggcccctgg cttgcgctcc cgaagaggag agcaaggctg ttctgggatc cggccgtcgt 180  
 gcggcaagag gcttgctctgt ccgggttgcc ggaaccagga gaacccagag ggaaaccgag 240  
 gcaaaggagc ggcgcggttt actagagaga gcgcgagcgg aagaggcgag agcaggagcg 300  
 cgcgagggag catcgagcgc agcggagac atg agg acc tac tgg ctg cac agc 353  
 Met Arg Thr Tyr Trp Leu His Ser  
 -20  
 gtc tgg gtg ctg ggc ttt ttc ctg tcc ctc ttc tca ttg caa gga ctg 401  
 Val Trp Val Leu Gly Phe Phe Leu Ser Leu Phe Ser Leu Gln Gly Leu  
 -15 -10 -5 1  
 cct gtt cgc agc gtg gat ttt aac cga ggc acg gac aac atc acc gtg 449  
 Pro Val Arg Ser Val Asp Phe Asn Arg Gly Thr Asp Asn Ile Thr Val  
 5 10 15  
 agg cag ggg gac aca gcc atc ctc agg tgc gtt gta gaa gac aag aac 497  
 Arg Gln Gly Asp Thr Ala Ile Leu Arg Cys Val Val Glu Asp Lys Asn  
 20 25 30  
 tca aag gtg gcc tgg ttg aac cgt tct ggc atc att ttt gct gga cat 545  
 Ser Lys Val Ala Trp Leu Asn Arg Ser Gly Ile Ile Phe Ala Gly His  
 35 40 45  
 gac aag tgg tct ctg gac cca cgg gtt gag ctg gag aaa cgc cat tct 593  
 Asp Lys Trp Ser Leu Asp Pro Arg Val Glu Leu Glu Lys Arg His Ser  
 50 55 60 65  
 ctg gaa tac agc ctc cga atc cag aag gtg gat gtc tat gat gag ggt 641  
 Leu Glu Tyr Ser Leu Arg Ile Gln Lys Val Asp Val Tyr Asp Glu Gly  
 70 75 80  
 tcc tac act tgc tca gtt cag aca cag cat gag ccc aag acc tcc caa 689  
 Ser Tyr Thr Cys Ser Val Gln Thr Gln His Glu Pro Lys Thr Ser Gln  
 85 90 95  
 gtt tac ttg atc gta caa gtc cca cca aag atc tcc aat atc tcc tcg 737  
 Val Tyr Leu Ile Val Gln Val Pro Pro Lys Ile Ser Asn Ile Ser Ser  
 100 105 110  
 gat gtc act gtg aat gag ggc agc aac gtg act ctg gtc tgc atg gcc 785  
 Asp Val Thr Val Asn Glu Gly Ser Asn Val Thr Leu Val Cys Met Ala  
 115 120 125  
 aat ggc cgt cct gaa cct gtt atc acc tgg aga cac ctt aca cca act 833  
 Asn Gly Arg Pro Glu Pro Val Ile Thr Trp Arg His Leu Thr Pro Thr

130		135		140		145	
gga agg gaa ttt gaa gga gaa gaa gaa tat ctg gag atc ctt ggc atc							881
Gly Arg Glu Phe Glu Gly Glu Glu Glu Tyr Leu Glu Ile Leu Gly Ile							
	150		155		160		
acc agg gag cag tca ggc aaa tat gag tgc aaa gct gcc aac gag gtc							929
Thr Arg Glu Gln Ser Gly Lys Tyr Glu Cys Lys Ala Ala Asn Glu Val							
	165		170		175		
tcc tcg gcg gat gtc aaa caa gtc aag gtc act gtg aac tat cct ccc							977
Ser Ser Ala Asp Val Lys Gln Val Lys Val Thr Val Asn Tyr Pro Pro							
	180		185		190		
act atc aca gaa tcc aag agc aat gaa gcc acc aca gga cga caa gct							1025
Thr Ile Thr Glu Ser Lys Ser Asn Glu Ala Thr Thr Gly Arg Gln Ala							
	195		200		205		
tca ctc aaa tgt gag gcc tcg gca gtg cct gca cct gac ttt gag tgg							1073
Ser Leu Lys Cys Glu Ala Ser Ala Val Pro Ala Pro Asp Phe Glu Trp							
	210		215		220		225
tac cgg gat gac act agg ata aat agt gcc aat ggc ctt gag att aag							1121
Tyr Arg Asp Asp Thr Arg Ile Asn Ser Ala Asn Gly Leu Glu Ile Lys							
	230		235		240		
agc acg gag ggc cag tct tcc ctg acg gtg acc aac gtc act gag gag							1169
Ser Thr Glu Gly Gln Ser Ser Leu Thr Val Thr Asn Val Thr Glu Glu							
	245		250		255		
cac tac ggc aac tac acc tgt gtg gct gcc aac aag ctg ggg gtc acc							1217
His Tyr Gly Asn Tyr Thr Cys Val Ala Ala Asn Lys Leu Gly Val Thr							
	260		265		270		
aat gcc agc cta gtc ctt ttc aaa cgt gtt tta ccc aca atc ccc cac							1265
Asn Ala Ser Leu Val Leu Phe Lys Arg Val Leu Pro Thr Ile Pro His							
	275		280		285		
ccc att caa gaa att ggt acc acc gtg cac ttc aag caa aaa ggc atc							1313
Pro Ile Gln Glu Ile Gly Thr Thr Val His Phe Lys Gln Lys Gly Ile							
	290		295		300		305
ttc ctc tct gag tct cag agg ggt gag aca acc aag atc act ctc aac							1361
Phe Leu Ser Glu Ser Gln Arg Gly Glu Thr Thr Lys Ile Thr Leu Asn							
	310		315		320		
tgt gga aat cta ttc ttg cgg aac tta cat ccc acc agt gat caa gag							1409
Cys Gly Asn Leu Phe Leu Arg Asn Leu His Pro Thr Ser Asp Gln Glu							
	325		330		335		
cca cag aga tta tgg aca ctt tgt tgc tta ctc cca aga aag ggc cag							1457
Pro Gln Arg Leu Trp Thr Leu Cys Cys Leu Leu Pro Arg Lys Gly Gln							
	340		345		350		
cac cgt att tat ggc cag tgc tagaagggtcc tcaactgaagg caacagggaa							1508
His Arg Ile Tyr Gly Gln Cys							
	355		360				
gaggcagcca tgaatatata cttggaaaca ggatcatttg aggccttcaa gaaggcataa							1568
aatattgtcc ctttcagcct ttcttttctt ctcaatgccca cgattaccaa ttatgtttta							1628
atcttaagtg gctagtgtta tatgtgatac attatgcctt tgatatgtgg ttgaaaaaat							1688
aaggcatagc attgtttttt atttcaaaga caaaataaac tgccagtgtc accaaaaaaa							1748
aaaaaaaa							1757

<210> 38  
 <211> 383  
 <212> PRT  
 <213> Homo sapiens



<220>  
 <221> SIGNAL  
 <222> 1..23

<400> 38

Met	Arg	Thr	Tyr	Trp	Leu	His	Ser	Val	Trp	Val	Leu	Gly	Phe	Phe	Leu
			-20					-15					-10		
Ser	Leu	Phe	Ser	Leu	Gln	Gly	Leu	Pro	Val	Arg	Ser	Val	Asp	Phe	Asn
	-5					1					5				
Arg	Gly	Thr	Asp	Asn	Ile	Thr	Val	Arg	Gln	Gly	Asp	Thr	Ala	Ile	Leu
10					15					20					25
Arg	Cys	Val	Val	Glu	Asp	Lys	Asn	Ser	Lys	Val	Ala	Trp	Leu	Asn	Arg
				30					35					40	
Ser	Gly	Ile	Ile	Phe	Ala	Gly	His	Asp	Lys	Trp	Ser	Leu	Asp	Pro	Arg
		45						50					55		
Val	Glu	Leu	Glu	Lys	Arg	His	Ser	Leu	Glu	Tyr	Ser	Leu	Arg	Ile	Gln
	60						65					70			
Lys	Val	Asp	Val	Tyr	Asp	Glu	Gly	Ser	Tyr	Thr	Cys	Ser	Val	Gln	Thr
	75					80					85				
Gln	His	Glu	Pro	Lys	Thr	Ser	Gln	Val	Tyr	Leu	Ile	Val	Gln	Val	Pro
90					95					100					105
Pro	Lys	Ile	Ser	Asn	Ile	Ser	Ser	Asp	Val	Thr	Val	Asn	Glu	Gly	Ser
				110					115					120	
Asn	Val	Thr	Leu	Val	Cys	Met	Ala	Asn	Gly	Arg	Pro	Glu	Pro	Val	Ile
			125					130					135		
Thr	Trp	Arg	His	Leu	Thr	Pro	Thr	Gly	Arg	Glu	Phe	Glu	Gly	Glu	Glu
		140					145					150			
Glu	Tyr	Leu	Glu	Ile	Leu	Gly	Ile	Thr	Arg	Glu	Gln	Ser	Gly	Lys	Tyr
	155					160					165				
Glu	Cys	Lys	Ala	Ala	Asn	Glu	Val	Ser	Ser	Ala	Asp	Val	Lys	Gln	Val
170					175					180					185
Lys	Val	Thr	Val	Asn	Tyr	Pro	Pro	Thr	Ile	Thr	Glu	Ser	Lys	Ser	Asn
				190					195					200	
Glu	Ala	Thr	Thr	Gly	Arg	Gln	Ala	Ser	Leu	Lys	Cys	Glu	Ala	Ser	Ala
		205						210					215		
Val	Pro	Ala	Pro	Asp	Phe	Glu	Trp	Tyr	Arg	Asp	Asp	Thr	Arg	Ile	Asn
		220					225					230			
Ser	Ala	Asn	Gly	Leu	Glu	Ile	Lys	Ser	Thr	Glu	Gly	Gln	Ser	Ser	Leu
	235					240					245				
Thr	Val	Thr	Asn	Val	Thr	Glu	Glu	His	Tyr	Gly	Asn	Tyr	Thr	Cys	Val
250					255					260					265
Ala	Ala	Asn	Lys	Leu	Gly	Val	Thr	Asn	Ala	Ser	Leu	Val	Leu	Phe	Lys
			270						275					280	
Arg	Val	Leu	Pro	Thr	Ile	Pro	His	Pro	Ile	Gln	Glu	Ile	Gly	Thr	Thr
			285				290						295		
Val	His	Phe	Lys	Gln	Lys	Gly	Ile	Phe	Leu	Ser	Glu	Ser	Gln	Arg	Gly
	300						305					310			
Glu	Thr	Thr	Lys	Ile	Thr	Leu	Asn	Cys	Gly	Asn	Leu	Phe	Leu	Arg	Asn
	315					320					325				
Leu	His	Pro	Thr	Ser	Asp	Gln	Glu	Pro	Gln	Arg	Leu	Trp	Thr	Leu	Cys
330					335					340					345
Cys	Leu	Leu	Pro	Arg	Lys	Gly	Gln	His	Arg	Ile	Tyr	Gly	Gln	Cys	
				350					355					360	

<210> 39  
 <211> 2818  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..80

<220>  
 <221> CDS  
 <222> 81..1517

<220>  
 <221> 3'UTR  
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<220>  
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 <222> 2786..2791

<220>  
 <221> polyA\_site  
 <222> 2804..2818

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 ctgcggagtc agacggcgct atg tac gcc ctc ttc ctc ctg gcc agc ctc ctg 113  
 Met Tyr Ala Leu Phe Leu Leu Ala Ser Leu Leu  
 1 5 10  
 ggc gcg gct cta gcc ggc ccg gtc ctt gga ctg aaa gaa tgc acc agg 161  
 Gly Ala Ala Leu Ala Gly Pro Val Leu Gly Leu Lys Glu Cys Thr Arg  
 15 20 25  
 ggc tcg gca gtg tgg tgc cag aat gtg aag acg gcg tcc gac tgc ggg 209  
 Gly Ser Ala Val Trp Cys Gln Asn Val Lys Thr Ala Ser Asp Cys Gly  
 30 35 40  
 gca gtg aag cac tgc ctg cag acc gtt tgg aac aag cca aca gtg aaa 257  
 Ala Val Lys His Cys Leu Gln Thr Val Trp Asn Lys Pro Thr Val Lys  
 45 50 55  
 tcc ctt ccc tgc gac ata tgc aaa gac gtt gtc acc gca gct ggt gat 305  
 Ser Leu Pro Cys Asp Ile Cys Lys Asp Val Val Thr Ala Ala Gly Asp  
 60 65 70 75  
 atg ctg aag gac aat gcc act gag gag gag atc ctt gtt tac ttg gag 353  
 Met Leu Lys Asp Asn Ala Thr Glu Glu Glu Ile Leu Val Tyr Leu Glu  
 80 85 90  
 aag acc tgt gac tgg ctt ccg aaa ccg aac atg tct gct tca tgc aag 401  
 Lys Thr Cys Asp Trp Leu Pro Lys Pro Asn Met Ser Ala Ser Cys Lys  
 95 100 105  
 gag ata gtg gac tcc tac ctc cct gtc atc ctg gac atc att aaa gga 449  
 Glu Ile Val Asp Ser Tyr Leu Pro Val Ile Leu Asp Ile Ile Lys Gly  
 110 115 120  
 gaa atg agc cgt cct ggg gag gtg tgc tct gct ctc aac ctc tgc gag 497  
 Glu Met Ser Arg Pro Gly Glu Val Cys Ser Ala Leu Asn Leu Cys Glu  
 125 130 135

tct ctc cag aag cac cta gca gag ctg aat cac cag aag cag ctg gag	545
Ser Leu Gln Lys His Leu Ala Glu Leu Asn His Gln Lys Gln Leu Glu	
140 145 150 155	
tcc aat aag atc cca gag ctg gac atg act gag gtg gtg gcc ccc ttc	593
Ser Asn Lys Ile Pro Glu Leu Asp Met Thr Glu Val Val Ala Pro Phe	
160 165 170	
atg gcc aac atc cct ctc ctc ctc tac cct cag gac ggc ccc cgc agc	641
Met Ala Asn Ile Pro Leu Leu Leu Tyr Pro Gln Asp Gly Pro Arg Ser	
175 180 185	
aag ccc cag cca aag gat aat ggg gac gtt tgc cag gac tgc att cag	689
Lys Pro Gln Pro Lys Asp Asn Gly Asp Val Cys Gln Asp Cys Ile Gln	
190 195 200	
atg gtg act gac atc cag act gct gta cgg acc aac tcc acc ttt gtc	737
Met Val Thr Asp Ile Gln Thr Ala Val Arg Thr Asn Ser Thr Phe Val	
205 210 215	
cag gcc ttg gtg gaa cat gtc aag gag gag tgt gac cgc ctg ggc cct	785
Gln Ala Leu Val Glu His Val Lys Glu Glu Cys Asp Arg Leu Gly Pro	
220 225 230 235	
ggc atg gcc gac ata tgc aag aac tat atc agc cag tat tct gaa att	833
Gly Met Ala Asp Ile Cys Lys Asn Tyr Ile Ser Gln Tyr Ser Glu Ile	
240 245 250	
gct atc cag atg atg atg cac atg cag gat cag caa ccc aag gag atc	881
Ala Ile Gln Met Met Met His Met Gln Asp Gln Gln Pro Lys Glu Ile	
255 260 265	
tgt gcg ctg gtt ggg ttc tgt gat gag gtg aaa gag atg ccc atg cag	929
Cys Ala Leu Val Gly Phe Cys Asp Glu Val Lys Glu Met Pro Met Gln	
270 275 280	
act ctg gtc ccc gcc aaa gtg gcc tcc aag aat gtc atc cct gcc ctg	977
Thr Leu Val Pro Ala Lys Val Ala Ser Lys Asn Val Ile Pro Ala Leu	
285 290 295	
gaa ctg gtg gag ccc att aag aag cac gag gtc cca gca aag tct gat	1025
Glu Leu Val Glu Pro Ile Lys Lys His Glu Val Pro Ala Lys Ser Asp	
300 305 310 315	
gtt tac tgt gag gtg tgt gaa ttc ctg gtg aag gag gtg acc aag ctg	1073
Val Tyr Cys Glu Val Cys Glu Phe Leu Val Lys Glu Val Thr Lys Leu	
320 325 330	
att gac aac aac aag act gag aaa gaa ata ctc gac gct ttt gac aaa	1121
Ile Asp Asn Asn Lys Thr Glu Lys Glu Ile Leu Asp Ala Phe Asp Lys	
335 340 345	
atg tgc tcg aag ctg ccg aag tcc ctg tcg gaa gag tgc cag gag gtg	1169
Met Cys Ser Lys Leu Pro Lys Ser Leu Ser Glu Glu Cys Gln Glu Val	
350 355 360	
gtg gac acg tac ggc agc tcc atc ctg tcc atc ctg ctg gag gag gtc	1217
Val Asp Thr Tyr Gly Ser Ser Ile Leu Ser Ile Leu Leu Glu Glu Val	
365 370 375	
agc cct gag ctg gtg tgc agc atg ctg cac ctc tgc tct ggc acg cgg	1265
Ser Pro Glu Leu Val Cys Ser Met Leu His Leu Cys Ser Gly Thr Arg	
380 385 390 395	
ctg cct gca ctg acc gtt cac gtg act cag cca aag gac ggt ggc ttc	1313
Leu Pro Ala Leu Thr Val His Val Thr Gln Pro Lys Asp Gly Gly Phe	
400 405 410	
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Cys Glu Val Cys Lys Lys Leu Val Gly Tyr Leu Asp Arg Asn Leu Glu	
415 420 425	

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aaa aac agc acc aag cag gag atc ctg gct gct ctt gag aaa ggc tgc 1409
Lys Asn Ser Thr Lys Gln Glu Ile Leu Ala Ala Leu Glu Lys Gly Cys
      430                      435                      440
agc ttc ctg cca gac cct tac cag aag cag tgt gat cag ttt gtg gca 1457
Ser Phe Leu Pro Asp Pro Tyr Gln Lys Gln Cys Asp Gln Phe Val Ala
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gag tac gag ccc gtg ctg atc gag atc ctg gtg gag gta tgg atc ctt 1505
Glu Tyr Glu Pro Val Leu Ile Glu Ile Leu Val Glu Val Trp Ile Leu
460                      465                      470                      475
cct tcg tgt gct tgaaaattgg agcctgcccc tcggcccata agcccttggt 1557
Pro Ser Cys Ala
gggaactgag aagtgtatat ggggccaag ctactggtgc cagaacacag agacagcagc 1617
ccagtgcaat gctgtcgagc attgcaaacy ccatgtgtgg aactaggagg aggaatatc 1677
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 <212> PRT  
 <213> Homo sapiens

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Cys Gln Asn Val Lys Thr Ala Ser Asp Cys Gly Ala Val Lys His Cys
      35      40      45
Leu Gln Thr Val Trp Asn Lys Pro Thr Val Lys Ser Leu Pro Cys Asp
      50      55      60
Ile Cys Lys Asp Val Val Thr Ala Ala Gly Asp Met Leu Lys Asp Asn
65      70      75      80
Ala Thr Glu Glu Glu Ile Leu Val Tyr Leu Glu Lys Thr Cys Asp Trp
      85      90      95
Leu Pro Lys Pro Asn Met Ser Ala Ser Cys Lys Glu Ile Val Asp Ser
100      105      110

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Tyr	Leu	Pro	Val	Ile	Leu	Asp	Ile	Ile	Lys	Gly	Glu	Met	Ser	Arg	Pro	115	120	125
Gly	Glu	Val	Cys	Ser	Ala	Leu	Asn	Leu	Cys	Glu	Ser	Leu	Gln	Lys	His	130	135	140
Leu	Ala	Glu	Leu	Asn	His	Gln	Lys	Gln	Leu	Glu	Ser	Asn	Lys	Ile	Pro	145	150	155
Glu	Leu	Asp	Met	Thr	Glu	Val	Val	Ala	Pro	Phe	Met	Ala	Asn	Ile	Pro	165	170	175
Leu	Leu	Leu	Tyr	Pro	Gln	Asp	Gly	Pro	Arg	Ser	Lys	Pro	Gln	Pro	Lys	180	185	190
Asp	Asn	Gly	Asp	Val	Cys	Gln	Asp	Cys	Ile	Gln	Met	Val	Thr	Asp	Ile	195	200	205
Gln	Thr	Ala	Val	Arg	Thr	Asn	Ser	Thr	Phe	Val	Gln	Ala	Leu	Val	Glu	210	215	220
His	Val	Lys	Glu	Glu	Cys	Asp	Arg	Leu	Gly	Pro	Gly	Met	Ala	Asp	Ile	225	230	235
Cys	Lys	Asn	Tyr	Ile	Ser	Gln	Tyr	Ser	Glu	Ile	Ala	Ile	Gln	Met	Met	245	250	255
Met	His	Met	Gln	Asp	Gln	Gln	Pro	Lys	Glu	Ile	Cys	Ala	Leu	Val	Gly	260	265	270
Phe	Cys	Asp	Glu	Val	Lys	Glu	Met	Pro	Met	Gln	Thr	Leu	Val	Pro	Ala	275	280	285
Lys	Val	Ala	Ser	Lys	Asn	Val	Ile	Pro	Ala	Leu	Glu	Leu	Val	Glu	Pro	290	295	300
Ile	Lys	Lys	His	Glu	Val	Pro	Ala	Lys	Ser	Asp	Val	Tyr	Cys	Glu	Val	305	310	315
Cys	Glu	Phe	Leu	Val	Lys	Glu	Val	Thr	Lys	Leu	Ile	Asp	Asn	Asn	Lys	325	330	335
Thr	Glu	Lys	Glu	Ile	Leu	Asp	Ala	Phe	Asp	Lys	Met	Cys	Ser	Lys	Leu	340	345	350
Pro	Lys	Ser	Leu	Ser	Glu	Glu	Cys	Gln	Glu	Val	Val	Asp	Thr	Tyr	Gly	355	360	365
Ser	Ser	Ile	Leu	Ser	Ile	Leu	Leu	Glu	Glu	Val	Ser	Pro	Glu	Leu	Val	370	375	380
Cys	Ser	Met	Leu	His	Leu	Cys	Ser	Gly	Thr	Arg	Leu	Pro	Ala	Leu	Thr	385	390	395
Val	His	Val	Thr	Gln	Pro	Lys	Asp	Gly	Gly	Phe	Cys	Glu	Val	Cys	Lys	405	410	415
Lys	Leu	Val	Gly	Tyr	Leu	Asp	Arg	Asn	Leu	Glu	Lys	Asn	Ser	Thr	Lys	420	425	430
Gln	Glu	Ile	Leu	Ala	Ala	Leu	Glu	Lys	Gly	Cys	Ser	Phe	Leu	Pro	Asp	435	440	445
Pro	Tyr	Gln	Lys	Gln	Cys	Asp	Gln	Phe	Val	Ala	Glu	Tyr	Glu	Pro	Val	450	455	460
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<211> 770

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<220>

<221> polyA\_site

<222> 755..770

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atg gag ctc tgc cgg tcc ctg gcc ctg ctg ggg ggc tcc ctg ggc ctg 168
Met Glu Leu Cys Arg Ser Leu Ala Leu Leu Gly Gly Ser Leu Gly Leu
-35 -30 -25
atg ttc tgc ctg att gct ttg agc acc gat ttc tgg ttt gag gct gtg 216
Met Phe Cys Leu Ile Ala Leu Ser Thr Asp Phe Trp Phe Glu Ala Val
-20 -15 -10
ggg ccc acc cac tca gct cac tcg ggc ctc tgg cca aca ggg cat ggg 264
Gly Pro Thr His Ser Ala His Ser Gly Leu Trp Pro Thr Gly His Gly
-5 1 5 10
gac atc ata tca ggc cac ggc ccg ctt gtc tca acc acc gca gcc ttt 312
Asp Ile Ile Ser Gly His Gly Pro Leu Val Ser Thr Thr Ala Ala Phe
15 20 25
gct gca ggt aag gac tct gga ctg gac tgg ggc atc gcg agc cag cga 360
Ala Ala Gly Lys Asp Ser Gly Leu Asp Trp Gly Ile Ala Ser Gln Arg
30 35 40
att cct gcc gag gag ctg agc cat ctc tct tgt cct tgt ccc cag cca 408
Ile Pro Ala Glu Glu Leu Ser His Leu Ser Cys Pro Cys Pro Gln Pro
45 50 55
tct cca tgg tgg tgg cca tgg cgg tgt aca cca gcg agc ggt ggg acc 456
Ser Pro Trp Trp Trp Pro Trp Arg Cys Thr Pro Ala Ser Gly Gly Thr
60 65 70 75
agc ctc cac acc ccc aga tcc aga cct tct tct cct ggt cct tct acc 504
Ser Leu His Thr Pro Arg Ser Arg Pro Ser Ser Pro Gly Pro Ser Thr
80 85 90
tgg gct ggg tct cag cta tcc tct tgc tct gta cag gtg ccc 546
Trp Ala Gly Ser Gln Leu Ser Ser Cys Ser Val Gln Val Pro
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 <222> 1..37

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           -20                          -15                          -10  
 Gly Pro Thr His Ser Ala His Ser Gly Leu Trp Pro Thr Gly His Gly  
           -5                          1                          5                          10  
 Asp Ile Ile Ser Gly His Gly Pro Leu Val Ser Thr Thr Ala Ala Phe  
                           15                          20                          25  
 Ala Ala Gly Lys Asp Ser Gly Leu Asp Trp Gly Ile Ala Ser Gln Arg  
           30                          35                          40  
 Ile Pro Ala Glu Glu Leu Ser His Leu Ser Cys Pro Cys Pro Gln Pro  
           45                          50                          55  
 Ser Pro Trp Trp Trp Pro Trp Arg Cys Thr Pro Ala Ser Gly Gly Thr  
           60                          65                          70                          75  
 Ser Leu His Thr Pro Arg Ser Arg Pro Ser Ser Pro Gly Pro Ser Thr  
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 Trp Ala Gly Ser Gln Leu Ser Ser Cys Ser Val Gln Val Pro  
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 <222> 1232..1237

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 <222> 1255..1340

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ccccactagg tgaag atg tca gcc cag gag agc tgc ctc agc ctc atc aag 171
Met Ser Ala Gln Glu Ser Cys Leu Ser Leu Ile Lys
1 5 10
tac ttc ctc ttc gtt ttc aac ctc ttc ttc ttc gtc ctc ggc agc ctg 219
Tyr Phe Leu Phe Val Phe Asn Leu Phe Phe Phe Val Leu Gly Ser Leu
15 20 25
atc ttc tgc ttc ggc atc tgg atc ctc att gac aag acc agc ttc gtg 267
Ile Phe Cys Phe Gly Ile Trp Ile Leu Ile Asp Lys Thr Ser Phe Val
30 35 40
tcc ttt gtg ggc ttg gcc ttc gtg cct ctg cag atc tgg tcc aaa gtc 315
Ser Phe Val Gly Leu Ala Phe Val Pro Leu Gln Ile Trp Ser Lys Val
45 50 55 60
ctg gcc atc tca gga atc ttc acc atg ggc atc gcc ctc ctg ggt tgt 363
Leu Ala Ile Ser Gly Ile Phe Thr Met Gly Ile Ala Leu Leu Gly Cys
65 70 75
gtg ggg gcc ctc aag gag ctc cgc tgc ctc ctg ggc ctg tat ttt ggg 411
Val Gly Ala Leu Lys Glu Leu Arg Cys Leu Leu Gly Leu Tyr Phe Gly
80 85 90
atg ctg ctg ctc ctg ttt gcc aca cag atc acc ctg gga atc ctc atc 459
Met Leu Leu Leu Leu Phe Ala Thr Gln Ile Thr Leu Gly Ile Leu Ile
95 100 105
tcc act cag cgg gcc agc tgg agc gaa gct tgc ggg acg tcg 501
Ser Thr Gln Arg Ala Ser Trp Ser Glu Ala Cys Gly Thr Ser
110 115 120
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<211> 122  
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<213> Homo sapiens

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20 25 30  
Gly Ile Trp Ile Leu Ile Asp Lys Thr Ser Phe Val Ser Phe Val Gly  
35 40 45  
Leu Ala Phe Val Pro Leu Gln Ile Trp Ser Lys Val Leu Ala Ile Ser



50		55		60
Gly Ile Phe Thr Met	Gly Ile Ala Leu Leu	Gly Cys Val Gly Ala Leu		
65	70	75	80	
Lys Glu Leu Arg Cys	Leu Leu Gly Leu Tyr	Phe Gly Met Leu Leu Leu		
	85	90	95	
Leu Phe Ala Thr Gln Ile Thr	Leu Gly Ile Leu Ile Ser Thr Gln Arg			
	100	105	110	
Ala Ser Trp Ser Glu Ala Cys	Gly Thr Ser			
	115	120		

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<220>  
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<220>  
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 <222> 1956..1999

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 atg cgc ctc cgc cgc cta gcg ctg ttc ccg ggt gtg gcg ctg ctt ctt 165  
 Met Arg Leu Arg Arg Leu Ala Leu Phe Pro Gly Val Ala Leu Leu Leu  
 -20 -15 -10  
 gcc gcg gcc cgc ctc gcc gct gcc tcc gac gtg cta gaa ctc acg gac 213  
 Ala Ala Ala Arg Leu Ala Ala Ala Ser Asp Val Leu Glu Leu Thr Asp  
 -5 1 5  
 gac aac ttc gag agt cgc atc tcc gac acg ggc tct gcg ggc ctc atg 261  
 Asp Asn Phe Glu Ser Arg Ile Ser Asp Thr Gly Ser Ala Gly Leu Met  
 10 15 20  
 ctc gtc gag ttc ttc gct ccc tgg tgt gga cac tgc aag aga ctt gca 309  
 Leu Val Glu Phe Phe Ala Pro Trp Cys Gly His Cys Lys Arg Leu Ala  
 25 30 35 40  
 cct gag tat gaa gct gca gct acc aga tta aaa gga ata gtc cca tta 357  
 Pro Glu Tyr Glu Ala Ala Ala Thr Arg Leu Lys Gly Ile Val Pro Leu  
 45 50 55  
 gca aag gtt gat tgc act gcc aac act aac acc tgt aat aaa tat gga 405

Ala	Lys	Val	Asp	Cys	Thr	Ala	Asn	Thr	Asn	Thr	Cys	Asn	Lys	Tyr	Gly		
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Val	Ser	Gly	Tyr	Pro	Thr	Leu	Lys	Ile	Phe	Arg	Asp	Gly	Glu	Glu	Ala		
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ggg	gct	tat	gat	gga	cct	agg	act	gct	gat	gga	att	gtc	agc	cac	ttg	501	
Gly	Ala	Tyr	Asp	Gly	Pro	Arg	Thr	Ala	Asp	Gly	Ile	Val	Ser	His	Leu		
	90					95					100						
aag	aag	cag	gca	gga	cca	gct	tca	gtg	cct	ctc	agg	act	gag	gaa	gaa	549	
Lys	Lys	Gln	Ala	Gly	Pro	Ala	Ser	Val	Pro	Leu	Arg	Thr	Glu	Glu	Glu		
105					110					115					120		
ttt	aag	aaa	ttc	att	agt	gat	aaa	gat	gcc	tct	ata	gta	ggg	ttt	ttc	597	
Phe	Lys	Lys	Phe	Ile	Ser	Asp	Lys	Asp	Ala	Ser	Ile	Val	Gly	Phe	Phe		
			125						130					135			
gat	gat	tca	ttc	agt	gag	gct	cac	tcc	gag	ttc	cta	aaa	gca	gcc	agc	645	
Asp	Asp	Ser	Phe	Ser	Glu	Ala	His	Ser	Glu	Phe	Leu	Lys	Ala	Ala	Ser		
			140					145					150				
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Asn	Leu	Arg	Asp	Asn	Tyr	Arg	Phe	Ala	His	Thr	Asn	Val	Glu	Ser	Leu		
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gtg	aac	gag	tat	gat	gat	aat	gga	gag	ggg	atc	atc	tta	ttt	cgt	cct	741	
Val	Asn	Glu	Tyr	Asp	Asp	Asn	Gly	Glu	Gly	Ile	Ile	Leu	Phe	Arg	Pro		
	170					175					180						
tca	cat	ctc	act	aac	aag	ttt	gag	gac	aag	act	gtg	gca	tat	aca	gag	789	
Ser	His	Leu	Thr	Asn	Lys	Phe	Glu	Asp	Lys	Thr	Val	Ala	Tyr	Thr	Glu		
185					190					195					200		
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Gln	Lys	Met	Thr	Ser	Gly	Lys	Ile	Lys	Lys	Phe	Ile	Gln	Glu	Asn	Ile		
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Phe	Gly	Ile	Cys	Pro	His	Met	Thr	Glu	Asp	Asn	Lys	Asp	Leu	Ile	Gln		
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Gly	Lys	Asp	Leu	Leu	Ile	Ala	Tyr	Tyr	Asp	Val	Asp	Tyr	Glu	Lys	Asn		
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gct	aaa	ggg	tcc	aac	tac	agg	aga	aac	agg	gta	atg	atg	gtg	gca	aag	981	
Ala	Lys	Gly	Ser	Asn	Tyr	Arg	Arg	Asn	Arg	Val	Met	Met	Val	Ala	Lys		
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Lys	Phe	Leu	Asp	Ala	Gly	His	Lys	Leu	Asn	Phe	Ala	Val	Ala	Ser	Arg		
265					270					275					280		
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Lys	Thr	Phe	Ser	His	Glu	Leu	Ser	Asp	Phe	Gly	Leu	Glu	Ser	Thr	Ala		
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Gly	Glu	Ile	Pro	Val	Val	Ala	Ile	Arg	Thr	Ala	Lys	Gly	Glu	Lys	Phe		
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Val	Met	Gln	Glu	Glu	Phe	Ser	Arg	Asp	Gly	Lys	Ala	Leu	Glu	Arg	Phe		
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Leu	Gln	Asp	Tyr	Phe	Asp	Gly	Asn	Leu	Lys	Arg	Tyr	Leu	Lys	Ser	Glu		
	330					335					340						
cct	atc	cca	gag	agc	aat	gat	ggg	cct	gtg	aag	gta	gtg	gta	gca	gag	1269	



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	90					95					100				
Lys	Lys	Gln	Ala	Gly	Pro	Ala	Ser	Val	Pro	Leu	Arg	Thr	Glu	Glu	Glu
105					110					115					120
Phe	Lys	Lys	Phe	Ile	Ser	Asp	Lys	Asp	Ala	Ser	Ile	Val	Gly	Phe	Phe
			125						130					135	
Asp	Asp	Ser	Phe	Ser	Glu	Ala	His	Ser	Glu	Phe	Leu	Lys	Ala	Ala	Ser
		140						145					150		
Asn	Leu	Arg	Asp	Asn	Tyr	Arg	Phe	Ala	His	Thr	Asn	Val	Glu	Ser	Leu
	155						160					165			
Val	Asn	Glu	Tyr	Asp	Asp	Asn	Gly	Glu	Gly	Ile	Ile	Leu	Phe	Arg	Pro
	170					175					180				
Ser	His	Leu	Thr	Asn	Lys	Phe	Glu	Asp	Lys	Thr	Val	Ala	Tyr	Thr	Glu
185				190					195						200
Gln	Lys	Met	Thr	Ser	Gly	Lys	Ile	Lys	Lys	Phe	Ile	Gln	Glu	Asn	Ile
			205					210						215	
Phe	Gly	Ile	Cys	Pro	His	Met	Thr	Glu	Asp	Asn	Lys	Asp	Leu	Ile	Gln
		220						225					230		
Gly	Lys	Asp	Leu	Leu	Ile	Ala	Tyr	Tyr	Asp	Val	Asp	Tyr	Glu	Lys	Asn
		235					240					245			
Ala	Lys	Gly	Ser	Asn	Tyr	Arg	Arg	Asn	Arg	Val	Met	Met	Val	Ala	Lys
	250					255					260				
Lys	Phe	Leu	Asp	Ala	Gly	His	Lys	Leu	Asn	Phe	Ala	Val	Ala	Ser	Arg
265				270						275					280
Lys	Thr	Phe	Ser	His	Glu	Leu	Ser	Asp	Phe	Gly	Leu	Glu	Ser	Thr	Ala
			285					290						295	
Gly	Glu	Ile	Pro	Val	Val	Ala	Ile	Arg	Thr	Ala	Lys	Gly	Glu	Lys	Phe
		300						305					310		
Val	Met	Gln	Glu	Glu	Phe	Ser	Arg	Asp	Gly	Lys	Ala	Leu	Glu	Arg	Phe
	315					320						325			
Leu	Gln	Asp	Tyr	Phe	Asp	Gly	Asn	Leu	Lys	Arg	Tyr	Leu	Lys	Ser	Glu
	330				335						340				
Pro	Ile	Pro	Glu	Ser	Asn	Asp	Gly	Pro	Val	Lys	Val	Val	Val	Ala	Glu
345				350						355					360
Asn	Phe	Asp	Glu	Ile	Val	Asn	Asn	Glu	Asn	Lys	Asp	Val	Leu	Ile	Glu
			365					370						375	
Phe	Tyr	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Asn	Leu	Glu	Pro	Lys	Tyr
		380					385						390		
Lys	Glu	Leu	Gly	Glu	Lys	Leu	Ser	Lys	Asp	Pro	Asn	Ile	Val	Ile	Ala
	395					400						405			
Lys	Met	Asp	Ala	Thr	Ala	Asn	Asp	Val	Pro	Ser	Pro	Tyr	Glu	Val	Arg
	410					415					420				
Gly	Phe	Pro	Thr	Ile	Tyr	Phe	Ser	Pro	Ala	Asn	Lys	Lys	Leu	Asn	Pro
425				430						435					440
Lys	Lys	Tyr	Glu	Gly	Gly	Arg	Glu	Leu	Ser	Asp	Phe	Ile	Ser	Tyr	Leu
			445					450						455	
Gln	Arg	Glu	Ala	Thr	Ile	Pro	Pro	Val	Ile	Gln	Glu	Glu	Lys	Pro	Lys
		460						465					470		
Lys	Lys	Lys	Lys	Ala	Gln	Glu	Asp	Leu							
	475						480								

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 <212> DNA  
 <213> Homo sapiens

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<220>  
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 gatgctgtgg ttgatatttt agaggacatt atc atg gat gac gag ttc cag tta 174  
 Met Asp Asp Glu Phe Gln Leu  
 1 5  
 tta cag aga aat ttc atg gac aag tac tac ctg gag ttt gaa gac aca 222  
 Leu Gln Arg Asn Phe Met Asp Lys Tyr Tyr Leu Glu Phe Glu Asp Thr  
 10 15 20  
 gaa gag aat aaa ctc atc tac aca cct att ttt aat gaa tac att tct 270  
 Glu Glu Asn Lys Leu Ile Tyr Thr Pro Ile Phe Asn Glu Tyr Ile Ser  
 25 30 35  
 ttg gta gaa aaa tac att gaa gaa cag ctg ctg cag cgg att cct gag 318  
 Leu Val Glu Lys Tyr Ile Glu Glu Gln Leu Leu Gln Arg Ile Pro Glu  
 40 45 50 55  
 ttc aac atg gca gcc ttc acc aca aca tta cag cac cat aag gat gaa 366  
 Phe Asn Met Ala Ala Phe Thr Thr Thr Leu Gln His His Lys Asp Glu  
 60 65 70  
 gtg gct ggt gac ata ttc gac atg ctg ctc acc ttc aca gat ttt ctg 414  
 Val Ala Gly Asp Ile Phe Asp Met Leu Leu Thr Phe Thr Asp Phe Leu  
 75 80 85  
 gct ttt aaa gaa atg ttt ttg gac tac aga gca gaa aaa gaa ggc cga 462  
 Ala Phe Lys Glu Met Phe Leu Asp Tyr Arg Ala Glu Lys Glu Gly Arg  
 90 95 100  
 gga ctg gac tta agc agt ggc tta gtg gtg act tca ttg tgc aaa tca 510  
 Gly Leu Asp Leu Ser Ser Gly Leu Val Val Thr Ser Leu Cys Lys Ser  
 105 110 115  
 tct tct ctg cca gct tcc cag aac aat ctg cgg cac taggtcctac 556  
 Ser Ser Leu Pro Ala Ser Gln Asn Asn Leu Arg His  
 120 125 130  
 ctccagccaa tgaatgggat cattctggat gtcaccagcc caataggctc agctcatgat 616  
 gacagaacac atcttggaac gactgactct gttatgtaac tcttcattta tgtaagtat 676  
 taatagggtca aaaccaaata gacctaacc tcttggaact atttcaaaaa aaaaaaaaaa 736

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 796  
 aaaaaaaaaa aaaaaaaaaa aaaagaaaaa aaaaaaaaaat 836

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 <212> PRT  
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<400> 48  
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 1 5 10 15  
 Tyr Leu Glu Phe Glu Asp Thr Glu Glu Asn Lys Leu Ile Tyr Thr Pro  
 20 25 30  
 Ile Phe Asn Glu Tyr Ile Ser Leu Val Glu Lys Tyr Ile Glu Glu Gln  
 35 40 45  
 Leu Leu Gln Arg Ile Pro Glu Phe Asn Met Ala Ala Phe Thr Thr Thr  
 50 55 60  
 Leu Gln His His Lys Asp Glu Val Ala Gly Asp Ile Phe Asp Met Leu  
 65 70 75 80  
 Leu Thr Phe Thr Asp Phe Leu Ala Phe Lys Glu Met Phe Leu Asp Tyr  
 85 90 95  
 Arg Ala Glu Lys Glu Gly Arg Gly Leu Asp Leu Ser Ser Gly Leu Val  
 100 105 110  
 Val Thr Ser Leu Cys Lys Ser Ser Ser Leu Pro Ala Ser Gln Asn Asn  
 115 120 125  
 Leu Arg His  
 130

<210> 49  
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 <212> DNA  
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<220>  
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 cggaggcagc tggggagggtc cgagcgatgt gaccaggccg ccacgcgtcg tctcttcctc 120  
 tctcctgccg cctcctgtct cgtaaataac ttttttactc taaagaaaga aagacaaaag 180  
 tagtcgtccg ccccc atg cat ccc ttc tac acc cgg gcc gcc acc atg ata 231

	Met	His	Pro	Phe	Tyr	Thr	Arg	Ala	Ala	Thr	Met	Ile	
	1				5					10			
ggc gag atc gcc gcc gtg tcc ttc atc tcc aag ttt ctc cgc acc													279
Gly Glu Ile Ala Ala Ala Val Ser Phe Ile Ser Lys Phe Leu Arg Thr													
	15				20					25			
aag ggg ctc acg agc gag cga cag ctg cag acc ttc agc cag agc ctg													327
Lys Gly Leu Thr Ser Glu Arg Gln Leu Gln Thr Phe Ser Gln Ser Leu													
	30				35					40			
cag gag ctg ctg gca gaa cat tat aaa cat cac tgg ttc cca gaa aag													375
Gln Glu Leu Leu Ala Glu His Tyr Lys His His Trp Phe Pro Glu Lys													
	45				50					55			60
cca tgc aag gga tgc ggt tac cgt tgt att cgc atc aac cat aaa atg													423
Pro Cys Lys Gly Ser Gly Tyr Arg Cys Ile Arg Ile Asn His Lys Met													
	65									70			75
gat cct ctg att gga cag gca gca cag cgg att gga ctg agc agt cag													471
Asp Pro Leu Ile Gly Gln Ala Ala Gln Arg Ile Gly Leu Ser Ser Gln													
	80									85			90
gag ctg ttc agg ctt ctc cca agt gaa ctc aca ctc tgg gtt gac ccc													519
Glu Leu Phe Arg Leu Leu Pro Ser Glu Leu Thr Leu Trp Val Asp Pro													
	95									100			105
tat gaa gtg tcc tac aga att gga gag gat ggc tcc atc tgt gtg ctg													567
Tyr Glu Val Ser Tyr Arg Ile Gly Glu Asp Gly Ser Ile Cys Val Leu													
	110									115			120
tat gaa gcc tca cca gca gga ggt agc act caa aac agc acc aac gtg													615
Tyr Glu Ala Ser Pro Ala Gly Gly Ser Thr Gln Asn Ser Thr Asn Val													
	125									130			135
caa atg gta gac agc cga atc agc tgt aag gag gaa ctt ctc ttg ggc													663
Gln Met Val Asp Ser Arg Ile Ser Cys Lys Glu Glu Leu Leu Leu Gly													
	145									150			155
aga acg agc cct tcc aaa aac tac aat atg atg act gta tca agt													708
Arg Thr Ser Pro Ser Lys Asn Tyr Asn Met Met Thr Val Ser Ser													
	160									165			170
taagatatag tctgtggatg gatcatctga tgatgatgga taaatttgat ttttgctttg													768
ggtagggctcc tcttggggat ggattatgga atttaaacca tgtcacagct gtgaagatct													828
ggcacaagat agaatggcaa aaaaaaaaaa aaaa													862

<210> 50

<211> 171

<212> PRT

<213> Homo sapiens

<400> 50

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Ala	Ala	Val	Ser	Phe	Ile	Ser	Lys	Phe	Leu	Arg	Thr	Lys	Gly	Leu	Thr
		20							25				30		
Ser	Glu	Arg	Gln	Leu	Gln	Thr	Phe	Ser	Gln	Ser	Leu	Gln	Glu	Leu	Leu
		35							40				45		
Ala	Glu	His	Tyr	Lys	His	His	Trp	Phe	Pro	Glu	Lys	Pro	Cys	Lys	Gly
		50							55				60		
Ser	Gly	Tyr	Arg	Cys	Ile	Arg	Ile	Asn	His	Lys	Met	Asp	Pro	Leu	Ile
		65							70				75		80
Gly	Gln	Ala	Ala	Gln	Arg	Ile	Gly	Leu	Ser	Ser	Gln	Glu	Leu	Phe	Arg
				85					90					95	

Leu	Leu	Pro	Ser	Glu	Leu	Thr	Leu	Trp	Val	Asp	Pro	Tyr	Glu	Val	Ser
			100					105					110		
Tyr	Arg	Ile	Gly	Glu	Asp	Gly	Ser	Ile	Cys	Val	Leu	Tyr	Glu	Ala	Ser
		115					120					125			
Pro	Ala	Gly	Gly	Ser	Thr	Gln	Asn	Ser	Thr	Asn	Val	Gln	Met	Val	Asp
	130					135					140				
Ser	Arg	Ile	Ser	Cys	Lys	Glu	Glu	Leu	Leu	Leu	Gly	Arg	Thr	Ser	Pro
145					150					155					160
Ser	Lys	Asn	Tyr	Asn	Met	Met	Thr	Val	Ser	Ser					
				165					170						

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 <212> DNA  
 <213> Homo sapiens

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 <222> 779..947

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 <221> polyA\_signal  
 <222> 912..917

<220>  
 <221> polyA\_site  
 <222> 932..947

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 a atg cca ctc ccc ctc cca tca gcg ttc gtg ctg tca gcc ttg cag cct 109  
 Met Pro Leu Pro Leu Pro Ser Ala Phe Val Leu Ser Ala Leu Gln Pro  
 -20 -15 -10  
 tct cct act cat tcc agc tcc aat acc cag cgg ctg cca gac cga gtg 157  
 Ser Pro Thr His Ser Ser Ser Asn Thr Gln Arg Leu Pro Asp Arg Val  
 -5 1 5 10  
 acc ggc ggc ttc tca gtg aat gga cag ctc att ggc aac aag gcc agg 205  
 Thr Gly Gly Phe Ser Val Asn Gly Gln Leu Ile Gly Asn Lys Ala Arg  
 15 20 25  
 agc cct ggg cag cat gac ggc acg tac ttc ggg cgg ctg gga atc gca 253  
 Ser Pro Gly Gln His Asp Gly Thr Tyr Phe Gly Arg Leu Gly Ile Ala  
 30 35 40  
 aac cct gcc acg gac ttt cag ttg gaa gtg act cct cag aac att acg 301  
 Asn Pro Ala Thr Asp Phe Gln Leu Glu Val Thr Pro Gln Asn Ile Thr  
 45 50 55  
 ctg aac ccc ggc ttt ggt ggg cct gtg ttt tcc tgg agg gac caa gct 349



Leu	Asn	Pro	Gly	Phe	Gly	Gly	Pro	Val	Phe	Ser	Trp	Arg	Asp	Gln	Ala	
60					65					70					75	
gtg	ctg	cgg	cag	gac	ggg	gtg	gtg	gtg	acc	atc	aac	aag	aag	agg	aac	397
Val	Leu	Arg	Gln	Asp	Gly	Val	Val	Val	Thr	Ile	Asn	Lys	Lys	Arg	Asn	
			80						85					90		
ctg	gtg	gtg	tct	gtg	gac	gac	ggg	ggc	acc	ttt	gag	ggt	ggt	ttg	cac	445
Leu	Val	Val	Ser	Val	Asp	Asp	Gly	Gly	Thr	Phe	Glu	Val	Val	Leu	His	
			95					100					105			
cga	gtg	tgg	aag	ggg	agc	tcg	gtc	cac	cag	gac	ttc	ctg	ggc	ttc	tat	493
Arg	Val	Trp	Lys	Gly	Ser	Ser	Val	His	Gln	Asp	Phe	Leu	Gly	Phe	Tyr	
		110					115					120				
gtg	ctg	gac	agt	cat	cgg	atg	tca	gcc	cgg	acg	cac	ggg	ctg	ctg	ggg	541
Val	Leu	Asp	Ser	His	Arg	Met	Ser	Ala	Arg	Thr	His	Gly	Leu	Leu	Gly	
		125				130					135					
caa	ttt	ttc	cac	ccc	atc	ggg	ttt	gaa	gtg	tct	gac	atc	cac	cca	ggc	589
Gln	Phe	Phe	His	Pro	Ile	Gly	Phe	Glu	Val	Ser	Asp	Ile	His	Pro	Gly	
140					145					150					155	
tct	gac	ccc	aca	aag	cca	gat	gcc	acg	atg	gtg	gtg	agg	aac	cgc	cgg	637
Ser	Asp	Pro	Thr	Lys	Pro	Asp	Ala	Thr	Met	Val	Val	Arg	Asn	Arg	Arg	
				160					165					170		
ctc	acg	gtc	acc	agg	ggg	ttg	caa	aaa	gac	tac	agc	aag	gac	ccg	tgg	685
Leu	Thr	Val	Thr	Arg	Gly	Leu	Gln	Lys	Asp	Tyr	Ser	Lys	Asp	Pro	Trp	
			175					180					185			
cat	ggg	gcc	gag	gtg	tcc	tgc	tgg	ttc	att	cac	aac	aat	ggg	gct	gga	733
His	Gly	Ala	Glu	Val	Ser	Cys	Trp	Phe	Ile	His	Asn	Asn	Gly	Ala	Gly	
		190					195					200				
ctc	atc	gat	ggg	gcc	tac	act	gat	tat	atc	gtc	ccc	gac	atc	ttc		778
Leu	Ile	Asp	Gly	Ala	Tyr	Thr	Asp	Tyr	Ile	Val	Pro	Asp	Ile	Phe		
		205				210					215					
tgagccctct	ggccagcagc	cctgtcctcc	cccggggcca	aggcagagga	ggaggacgac											838
atcctgacct	gctgctgagg	ctgtacctcc	ttgactaagc	tggttccttg	tgtcaaagca											898
cctcatgcct	tccattaaag	agaggccgtg	tccaaaaaaa	aaaaaaaaaa												947

<210> 52

<211> 239

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..21

<400> 52

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Ser	Pro	Thr	His	Ser	Ser	Ser	Asn	Thr	Gln	Arg	Leu	Pro	Asp	Arg	Val	
-5				1				5					10			
Thr	Gly	Gly	Phe	Ser	Val	Asn	Gly	Gln	Leu	Ile	Gly	Asn	Lys	Ala	Arg	
			15				20					25				
Ser	Pro	Gly	Gln	His	Asp	Gly	Thr	Phe	Gly	Arg	Leu	Gly	Ile	Ala		
		30				35					40					
Asn	Pro	Ala	Thr	Asp	Phe	Gln	Leu	Glu	Val	Thr	Pro	Gln	Asn	Ile	Thr	
		45				50				55						
Leu	Asn	Pro	Gly	Phe	Gly	Gly	Pro	Val	Phe	Ser	Trp	Arg	Asp	Gln	Ala	

60					65				70				75
Val	Leu	Arg	Gln	Asp	Gly	Val	Val	Val	Thr	Ile	Asn	Lys	Arg
				80					85				90
Leu	Val	Val	Ser	Val	Asp	Asp	Gly	Gly	Thr	Phe	Glu	Val	Leu
			95					100					105
Arg	Val	Trp	Lys	Gly	Ser	Ser	Val	His	Gln	Asp	Phe	Leu	Gly
			110					115				120	
Val	Leu	Asp	Ser	His	Arg	Met	Ser	Ala	Arg	Thr	His	Gly	Leu
			125					130				135	
Gln	Phe	Phe	His	Pro	Ile	Gly	Phe	Glu	Val	Ser	Asp	Ile	His
140						145				150			155
Ser	Asp	Pro	Thr	Lys	Pro	Asp	Ala	Thr	Met	Val	Val	Arg	Asn
				160					165				170
Leu	Thr	Val	Thr	Arg	Gly	Leu	Gln	Lys	Asp	Tyr	Ser	Lys	Asp
			175					180					185
His	Gly	Ala	Glu	Val	Ser	Cys	Trp	Phe	Ile	His	Asn	Asn	Gly
			190					195				200	
Leu	Ile	Asp	Gly	Ala	Tyr	Thr	Asp	Tyr	Ile	Val	Pro	Asp	Ile
			205				210					215	